

GenCore version 5.1.8
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OMP:protein - protein search, using sw model
Run on: May 19, 2006, 17:34:57 ; Search time 158.667 Seconds
(without alignments)
391.900 Million cell updates/sec

Title: US-09-889-936A-6
Perfect score: 737
Sequence: 1 MRVLILLWLTAPPGLISDV.....WDYGTYYGYFVWGGQTTVT 136
Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5
Searched: 2589679 seqs, 457216429 residues
Total number of hits satisfying chosen parameters: 2589679

Minimum DB seq length: 0
Maximum DB seq length: 2000000000
Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : A_Geneseq.8:*
1: Geneseqp1980s:*
2: Geneseqp1990s:*
3: Geneseqp2000s:*
4: Geneseqp2001s:*
5: Geneseqp2002s:*
6: Geneseqp2003as:*
7: Geneseqp2003bs:*
8: Geneseqp2004s:*
9: Geneseqp2005s:*
10: Geneseqp2006s:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	737	100.0	136	3 AAB15672	Aab15672 Murine 5B
2	627.5	85.1	488	9 ADY91369	Ady91369 Anti-KID3
3	622.5	84.5	136	9 ADZ81889	Adz81889 Anti-lami
4	593.5	80.5	130	10 AEE98109	Aee98109 Murine PE
5	588.5	79.9	136	2 AAW01144	Aaw01144 Mab 1.4 h
6	588.5	79.9	136	2 AAW44169	Aaw44169 Monoclonal
7	588.5	79.8	137	2 AAR28671	Aar28671 pPM-h1 pr
8	586.5	79.6	134	6 ABB82796	Abb82796 Antibody
9	569.5	77.3	255	8 ADS14282	Ads14282 Murine pr
10	569.5	77.3	519	8 ADS14288	Ads14288 Murine pr
11	556.5	75.5	120	8 ADO44274	Ado44274 Consensus
12	556.5	75.5	120	8 ADO44271	Ado44271 Sequence
13	554	75.2	127	7 ADJ76886	Adj76886 Anti-IGF-
14	554	75.2	127	9 ADZ67056	Adz67056 Murine im
15	554	75.2	127	9 AEE61302	Aee61302 Murine mo
16	552.5	75.0	119	8 ADO44272	Ado44272 Primer in
17	544.5	73.9	120	8 ADO44280	Ado44280 Humanised
18	544.5	73.9	122	8 ADL26964	Adl26964 Mouse ant
19	544	73.8	121	6 ABP59986	Abp59986 Antibody
20	544	73.8	121	7 ADF69650	Adf69650 Humanised
21	544	73.8	121	9 AEB03869	Aeb03869 B-CLL pha
22	544	73.8	121	9 AEE17798	Aee17798 Anti-huma
23	541	73.4	119	2 AAW01584	Aaw01584 Lead bind

24	539.5	73.2	730	9 AEC08410	Aec08410 ScFv-B2-F
25	539.5	73.2	730	9 AEC08411	Aec08411 ScFv-B2-F
26	539.5	73.2	761	9 AEC08409	Aec08409 ScFv-A12A
27	539.5	73.2	762	9 AEC08408	Aec08408 ScFv-B2-F
28	537.5	72.9	154	9 AEE17974	Aee17974 Murine SC
29	535.5	72.7	140	2 AAW21937	Aaw21937 Variable
30	535.5	72.7	140	2 AAY05267	Aay05267 Antibody
31	535.5	72.7	140	5 ABG98318	Abg98318 Murine wi
32	533.5	72.4	539	8 ADR42630	Adr42630 Mouse ant
33	533	72.3	522	9 AEC20775	Aec20775 M-CSF spe
34	532.5	72.3	115	7 ADJ80371	Adj80371 Murine an
35	531.5	72.1	118	9 ADZ81874	Adz81874 Anti-lami
36	529.5	71.8	122	9 ADW14662	Adw14662 Anti-comp
37	529	71.8	126	2 AAR24722	Aar24722 Sequence
38	528.5	71.7	118	9 AEC20767	Aec20767 M-CSF spe
39	528.5	71.7	447	9 AEC20763	Aec20763 M-CSF spe
40	527.5	71.6	118	7 ADJ76904	Adj76904 Anti-IGF-
41	527.5	71.6	118	9 ADZ67074	Adz67074 Mouse ant
42	527.5	71.6	118	9 AEB61320	Aee61320 Murine mo
43	526.5	71.4	114	9 ADZ81898	Adz81898 Mouse ant
44	526	71.4	117	8 ADU39968	Adu39968 Antibody
45	525.5	71.3	117	2 AAR07318	Aar07318 VH domain

ALIGNMENTS

RESULT 1
AAB15672
ID AAB15672 standard; protein; 136 AA.
XX
AC AAB15672;
XX
DT 08-JAN-2001 (first entry)
XX
DE Murine 5B3 antibody heavy chain variable region.
XX
KW Mouse; 5B3 antibody; IgG1; piezoelectric immunoassay;
KW small molecule explosive detection; 2,4,6-trinitrotoluene; TNT.
XX
OS Mus sp.
XX
PN WO200043774-A2.
XX
PD 27-JUL-2000.
XX
PF 25-JAN-2000; 2000WO-IL000048.
XX
PR 25-JAN-1999; 99IL-00128212.
XX
(VISS) VISSUM RES & DEV CO.
(YEDA) YEDA RES & DEV CO LTD.
PI Willner I, Eshhar Z;
XX
DR WPI; 2000-524259/47.
DR N-PSDB; AAA74604.
XX
PT Apparatus for detecting small molecules, especially explosives comprises
PT a piezoelectric crystal.
XX
PS Disclosure; Fig 3A; 90pp; English.
XX
CC The present sequence is the heavy chain variable region of 5B3 antibody.
CC The cDNA encoding this sequence was obtained from total RNA extracted
CC from a 5B3 hybridoma by RT-PCR. 5B3 is an IgG1 antibody derived from a
CC TNP-KLH immunised mouse. Its binding to TNP or DNS antigen can be blocked
CC by very low amounts of TNT and it can therefore be used in a method for
CC detecting small assayed explosive molecules. Molecules are detected using
CC a piezoelectric sensor. Piezoelectric immunoassaying in liquid phase
CC allows stationary and flow analysis of an aqueous sample. The method is
CC sufficiently sensitive for detection of low molecular weight molecules

The invention relates to a peptide that competes with mAb 5D5, mAb 6C12, or cross-competes with both 5D5 and 6C12 in specifically binding to at least a portion of domain III of the gamma2 chain of human laminin-5 (Ln-5 gamma2 DIII). Also included are a composition comprising an amount of the isolated peptide and a pharmaceutical carrier, an assay for assessing the gamma2-associated peptide content of a composition (comprising administering the peptide to the composition and determining whether the peptide binds any gamma2-associated peptides in the composition), a method of reducing cancer progression in a patient and a method of treating cancer in a patient. The peptide is a monoclonal antibody, preferably a humanized antibody or a fully human antibody. It binds a protein that is secreted from human cancer cells and comprises at least a portion of Ln-5 gamma2 DIII. The peptide is also conjugated to a compound that kills cancer cells and/or to a detection agent. The peptide, nucleic acid comprising a sequence encoding the peptide, or both the peptide and the nucleic acid, and the composition are useful in the preparation of a medicament for the treatment of cancer. The peptides, nucleic acids, and composition are useful for diagnosing, treating, or preventing cancer. The present sequence represents a Anti-laminin-5 gamma2 antibody heavy chain.

CC polypeptide encoded by the PERP gene. The disease is cancer. The antibody
 CC is useful in diagnosing a disease by detecting or measuring the amount of
 CC a polypeptide encoded by the PERP gene in a cell, for treating cancer,
 CC for manufacturing a diagnostic, for detecting cancer and for
 CC manufacturing a therapeutic agent for cancer. This sequence represents a
 CC murine PERP related protein of the invention. Note: The sequence data for
 CC this patent did not form part of the printed specification, but was
 CC obtained in electronic format directly from WIPO at
 CC ftp.wipo.int/pub/published_pct_sequences.
 XX
 SQ Sequence 130 AA;

Query Match 80.5%; Score 593.5; DB 10; Length 130;
 Best Local Similarity 81.6%; Pred. No. 1.3e-47;
 Matches 111; Conservative 10; Mismatches 6; Indels 9; Gaps 1;
 QY 1 MRVLILLMLFTAPPGILSDVQLQESGPGVLKPSQSLTCSVTGYSITSGYAWNRIQPP 60
 DB |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
 1 MRVLILLMLFTAPPGILSDVQLQESGPGVLKPSQSLTCTVTGFSITTEYAWNRIQPP 60
 QY 61 GNKLEWMGYISYSGFTSYNPSLRISFTRDTSKNQFFLQLSNVTSEDTATYYCARWDYG 120
 DB |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
 61 GNRLEWMGYIGYTRTNYSPSLKRSIRITRDTSKNQFFLQLSNVTSEDTATYYCTRM DY- 119
 QY 121 TTYGYFDVWGQGT TTVT 136
 DB |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
 120 -----WGQGT TSVT 127

RESULT 5
 AA001144
 ID AAW01144 standard; protein; 136 AA.
 XX
 AC AAW01144;
 DT 10-FEB-1997 (first entry)
 DE MAB 1.4 heavy chain, directed against type II phospholipase A2.
 XX
 KW Monoclonal antibody; phospholipase; myocardial infarction; pancreatitis;
 KW cerebral infarction; acute kidney failure; colitis; chronic rheumatism;
 KW adult respiratory distress syndrome; cardiac shock; treatment;
 KW preclinical testing; disease; hybridoma.
 XX
 OS Mus musculus.

Key	Location/Qualifiers
Binding-site	49..54 /label= CDR 1
Binding-site	69..84 /label= CDR 2
Binding-site	117..125 /label= CDR 3
PN	WO9620959-A1.
PD	11-JUL-1996.
XX	
PF	27-DEC-1995; 95WO-JP002714.
PR	29-DEC-1994; 94JP-00340006.
XX	
PA	(YAMA) YAMANOUCHI PHARM CO LTD.
XX	
PI	Kawauchi Y, Takasaki J, Yasunaga T, Masuho Y;
XX	
WPI	1996-333946/33.
DR	N-PSDB; AAT40804.
XX	
XX	Monoclonal antibody inhibiting type II phospholipase A2 activity - for
PT	treatment of myocardial and cerebral infarction.
XX	
PS	Claim 6; Fig 11; 69pp; Japanese.

XX
 CC Monoclonal antibodies which inhibit type II phospholipase A2 are useful
 CC in the treatment of myocardial infarction, cerebral infarction, acute
 CC kidney failure, chronic rheumatism, cardiac shock, pancreatitis, adult
 CC respiratory distress syndrome and colitis. The antibodies were generated
 CC by immunising Balb/C mice with recombinant human type II phospholipase
 CC A2. Spleen cells from the mice were fused with mouse myeloma P3U1
 CC (P3x63Ag8.U1) and the hybridomas obtained were screened for phospholipase
 CC A2 inhibitory activity. Active clones were isolated including 12H5, 1.4
 CC and 10.1. These were cultured and the antibody isolated from the culture
 CC supernatant by precipitation with ammonium sulphate and purification on a
 CC column of protein A-Sepharose CL4B. Because the antibody acts on the
 CC primate and mouse forms of enzyme as well as human it is particularly
 CC suitable for preclinical testing
 XX
 SQ Sequence 136 AA;

Query Match 79.9%; Score 588.5; DB 2; Length 136;
 Best Local Similarity 81.4%; Pred. No. 4.1e-47;
 Matches 114; Conservative 4; Mismatches 11; Indels 11; Gaps 2;
 QY 1 MRVLILLMLFTAPPGILSDVQLQESGPGVLKPSQSLTCSVTGYSITSGYAWNRIQPP 60
 DB |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
 1 MRVLILLMLFTAPPGILSDVQLQESGPGVLKPSQSLTCTVTGFSITTEYAWNRIQPP 60
 QY 61 GNKLEWMGYISYSGFTSYNPSLRISFTRDTSKNQFFLQLSNVTSEDTATYYCAR---- 116
 DB |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
 61 GNRLEWMGYIRYSGYTSYNPSLRISFTRDTSKNQFFLQLSNVTSEDTATYYCTRD LDA 120
 QY 117 WDYGTYGYFDVWGQGT TTVT 136
 DB |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
 121 W-----YFDVWGAGT TTVT 133

RESULT 6
 AA044169
 ID AAW44169 standard; protein; 136 AA.
 XX
 AC AAW44169;
 DT 16-JUN-1998 (first entry)
 DE Monoclonal antibody 1.4 heavy chain against type II phospholipase A2.
 XX
 KW Monoclonal antibody; type II phospholipase A2; inhibition; cisplatin;
 KW amelioration; kidney disorder; nephrotoxicity; anticancer.
 XX
 OS Unidentified.

PN	WO9749427-A1.
PD	31-DEC-1997.
XX	
PF	27-JUN-1997; 97WO-JP002241.
PR	27-JUN-1996; 96JP-00167286.
PR	19-SEP-1996; 96JP-00247635.
XX	
PA	(YAMA) YAMANOUCHI PHARM CO LTD.
XX	
PI	Kawauchi Y, Takasaki J, Hayashi K, Masuho Y;
XX	
DR	WPI: 1998-076914/07.
DR	N-PSDB; AAV12261.
XX	
PT	Amelioration of kidney disorders caused by cisplatin administration - by
PT	treatment with an antibody inhibiting type II phospholipase A2 activity.
XX	
PS	Disclosure; Page 38; 74pp; Japanese.
XX	
CC	The present sequence represents the monoclonal antibody 1.4 heavy chain
CC	against type II phospholipase A2, from the present invention. The present
CC	invention describes a novel method for the amelioration of kidney

CC disorders (such as acute renal failure) associated with the
CC administration of cisplatin for the treatment of cancer. The method
CC comprises treatment with a monoclonal antibody which inhibits the
CC activity of type II phospholipase A2 (particularly of type II
CC phospholipase A2 of human origin), or with a protein or peptide
CC possessing the same inhibitory activity and containing a part of the
CC antibody sequence. Preferably the antibody also inhibits the activity of
CC ape and/or mouse type II phospholipase A2, and has the ability to release
CC type II phospholipase A2 bound to a cell membrane. Three specific
CC monoclonal antibodies having these properties which can be used are 12H5,
CC 10.1 and 1.4, derived from hybridomas FERM BP-5300, FERM BP-5298 and FERM
CC BP-5297 respectively. The method can be used for suppressing the
CC nephrotoxicity which is a characteristic feature of cisplatin
CC administration, and therefore allowing more efficient use of this drug as
CC an anticancer agent, e.g. by allowing an increased dosage to be used
XX
XX
SQ Sequence 136 AA;

Query Match 79.9%; Score 588.5; DB 2; Length 136;
Best Local Similarity 81.4%; Pred. No. 4.1e-47;
Matches 114; Conservative 4; Mismatches 11; Indels 11; Gaps 2;
QY 1 MRVLILLMLFTAPPGILSDVQLQESGPGVLKPSQSLTCSVTGYISITSGYAWNMIROPP 60
DB 1 MRVLILLMLFTAPPGILSDVQLQESGPGVLKPSQSLTCSVTGYISITSDYAWNMIROPP 60
QY 61 GNKLEMMGYISYSGTSYNPSLRISFTRDTSKNQFFLQLNSVTSEDTATYYCAR---- 116
DB 61 GNKLEMMGYIRSYGYTSYNPSLKSRIFFTRDTSQNQFFLHLTSVTEDTATYYCTRDLLA 120
QY 117 WDYGTYGYFDVWGQGTTVT 136
DB 121 W-----YFDVWGAGTTVT 133

RESULT 7
AAR28671
ID AAR28671 standard; protein; 137 AA.
XX AC AAR28671;
XX
DT 25-MAR-2003 (revised)
DT 30-MAR-1993 (first entry)
XX
DE pPM-h1 protein product.
XX Human; antibody; interleukin-6; receptor; IL-6R; light chain; L; H;
KW heavy chain; variable region; mouse; monoclonal; hybridoma; PM1; plasmid;
KW pPM-K3; pPM-h1.
XX
OS Synthetic.
FH Key Location/Qualifiers
FT Peptide 1..18 /note= "Signal peptide"
FT Protein 19..137 /note= "Mature peptide"
XX
XX WO9219759-A1.
XX
PD 12-NOV-1992.
XX
XX 24-APR-1992; 92WO-JP0000544.
XX
PR 25-APR-1991; 91JP-00095476.
PR 19-FEB-1992; 92JP-00032084.
XX
XX (CHUS) CHUGAI SEIYAKU KK.
XX
XX Tsuchiya M, Sato K, Bendig MM, Jones ST, Saldanha JW;
XX
XX WPI; 1992-398882/48.
DR N-PSDB; AAQ30756.

XX Reconstituted human antibody to human interleukin-6 receptor - has low
PT antigenicity and contains mouse V-region complementarily determining
PT regions.
XX
PS Disclosure; Page 122-123; 207pp; Japanese.
XX
CC The sequences given in AAR28670-71 were encoded by plasmids which were
CC used in example to illustrate the production of a human antibody which
CC recognises human interleukin-6 receptor (IL-6R). The antibody comprises
CC light (L) chain and heavy (H) chain variable regions which were derived
CC from a mouse monoclonal antibody produced from the hybridoma PM1 which
CC contained the plasmids pPM-K3 and pPM-h1. (Updated on 25-MAR-2003 to
CC correct PN field.)
XX
SQ Sequence 137 AA;

Query Match 79.8%; Score 588; DB 2; Length 137;
Best Local Similarity 83.8%; Pred. No. 4.6e-47;
Matches 114; Conservative 8; Mismatches 12; Indels 2; Gaps 1;
QY 1 MRVLILLMLFTAPPGILSDVQLQESGPGVLKPSQSLTCSVTGYISITSGYAWNMIROPP 60
DB 1 MRVLILLMLFTAPPGILSDVQLQESGPGVLKPSQSLTCTVTGYISITSDHAWMIROPP 60
QY 61 GNKLEMMGYISYSGTSYNPSLRISFTRDTSKNQFFLQLNSVTSEDTATYYCARWDYG 120
DB 61 GNKLEMMGYISYSGITTYNPSLKSRISTRDTSKNQFFLQLNSVTGDTSTYYCARSLAR 120
QY 121 TTYGYFDVWGQGTTVT 136
DB 121 TT--AMDYWGQGTSTVT 134

RESULT 8
ABB2796
ID ABB2796 standard; protein; 134 AA.
XX AC ABB2796;
XX
DT 18-MAR-2003 (first entry)
XX
DE Antibody 806 variable heavy chain (VH) region.
KW Epidermal growth factor receptor; EGFR; tumourigenic; cytostatic;
KW monoclonal antibody; mAb 806; antibody therapy; tumour.
XX
OS Homo sapiens.
FH Key Location/Qualifiers
FT Peptide 1..18 /note= "signal peptide"
FT Protein 19..134 /note= "mAb 806 VH region"
XX
XX WO200292771-A2.
XX
PD 21-NOV-2002.
XX
XX 13-MAY-2002; 2002WO-US015185.
XX
PR 11-MAY-2001; 2001US-0290410P.
PR 28-SEP-2001; 2001US-0326019P.
PR 21-DEC-2001; 2001US-0342258P.
XX
XX (LUDW-) LUDWIG INST CANCER RES.
XX
XX Old LJ, Johns TG, Panousis C, Scott AM, Renner C, Ritter G;
PI Jungbluth A, Stockert E, Collins P, Cavenee WK, Huang H, Burgess AW;
PI Nice EC;
XX
XX WPI; 2003-129282/12.
DR N-PSDB; ABZ23940.

XX Novel specific binding members, particularly antibodies recognizing
PT epidermal growth factor receptor epitope found only in tumorigenic cells,
PT useful for diagnosing, preventing and treating cancer in mammals.
XX
PS Claim 6; Fig 14B; 123pp; English.
XX
XX The invention relates to an isolated specific binding member (I) which
CC recognizes an epidermal growth factor receptor (EGFR) epitope which is
CC found in tumorigenic, hyperproliferative or abnormal cells and not
CC detectable in normal cells. The EGFR epitope is located within the region
CC comprising residues 273-501 of EGFR and does not demonstrate any amino
CC acid sequence alterations or substitutions from normal EGFR. (I) is
CC capable of binding the de2-7 EGFR at an epitope distinct from the
CC functional peptide and does not bind to EGFR on normal cells in the
CC absence of aberrant expression, or in the absence of amplification of
CC normal wild-type gene. The binding member comprises the VH and VL
CC polypeptide sequence of monoclonal antibody (mAb) 806. (I) is useful for
CC treating or diagnosing human or animal body, especially for treating
CC tumour in a human. (I) is useful for the preparation of a medicament and
CC for preventing or treating cancer which is located in or adjacent the
CC brain, in a mammal. (I) is also useful for detecting the presence of
CC amplified EGFR, de2-7EGFR or EGFR with high mannose glycosylation, where
CC the presence of amplified EGFR, de2-7EGFR or EGFR with a high mannose
CC glycosylation is suspected with (I) under conditions that allow binding
CC of the EGFR to the antibody to occur, and detecting whether binding has
CC occurred between the EGFR from the sample and the antibody, where the
CC detection of binding indicates that presence or activity of the EGFR in
CC the sample. This method is useful for detecting cancer in mammals by
CC detecting the presence or activity of an EGFR which indicates the
CC existence of a tumour or cancer in the mammal. A pharmaceutical
CC composition comprising (I), and optionally vehicle, carrier or diluent is
CC useful for preventing and/or treating cancer in mammals, especially for
CC treating brain-resident cancers that produce aberrantly expressed EGFR in
CC mammals, such as glioblastoma, medulloblastoma, meningioma, neoplastic
CC astrocytoma or neoplastic arteriovenous malformations, and malignant
CC neural tumours in mammals. The present sequence represents the mAb 806 VH
CC region
XX
SQ Sequence 134 AA;
Query Match 79.6%; Score 586.5; DB 6; Length 134;
Best Local Similarity 83.1%; Pred No. 6.2e-47;
Matches 113; Conservative 4; Mismatches 1; Indels 5; Gaps 1;
Qy 1 MRVLILLWLTAFPGILSDVQLQESGPGLVKPSQSLTCSVTGYSTSGYAWNWIRQFP 60
Db 1 MRVLILLWLTAFPGVLSVQLQESGPGSLVKPSQSLTCTVTGYSTSDFAWNWIRQFP 60
Qy 61 GNKLEWNGYISYSGFTSYNPSLSRISFTRDTSKNQFFLQNLNSVTSEDTATYYCARWDYG 120
Db 61 GNKLEWNGYISYSGNTRYNPSLSKRSISRTDTSKNQFFLQNLNSVTIEDTATYYCVTAGRG 120
Qy 121 TTYGYFDVWGGQTTVT 136
Db 121 -----FPWGGQTLVT 131
RESULT 9
ID ADS14282 standard; protein; 255 AA.
XX
AC ADS14282;
XX
DT 16-DEC-2004 (first entry)
XX
DE Murine protein relating to the invention SEQ ID NO:8.
XX variant receptor; antidiabetic; haemostatic; endocrine; thrombocytopenia;
KW type II diabetes; laron syndrome; thrombopoietin.
XX
OS Mus musculus.

XX WO2004081048-A1.
PN
XX 23-SEP-2004.
PD
XX
PF 12-MAR-2004; 2004WO-JP003334.
PP
XX
PR 13-MAR-2003; 2003JP-00067832.
PX
PA (CHUS) CHUGAI SEIYAKU KK.
XX
PI Tsuchiya M, Hirata Y;
XX
DR WPI; 2004-677525/66.
DR N-FSDB; ADS14281.
XX
XX Novel ligand having agonist activity with respect to variant receptor
PT e.g., variant thrombopoietin receptor, useful for treating disease
PT resulting due to variant receptor such as congenital non-megakaryocyte
PT thrombocytopenia.
XX
XX Example 4; SEQ ID NO 8; 132pp; Japanese.
PS
XX The invention relates to a novel ligand (preferably an antibody) (I)
CC having agonist activity with respect to a variant receptor. A ligand of
CC the invention has antidiabetic, haemostatic, and endocrine-gen. activity.
CC The ligand is useful for treating the disease caused due to variant
CC receptor, which involves combining the ligand/antibody with the variant
CC receptor, where the disease is congenital non-megakaryocyte
CC thrombocytopenia. A ligand of the invention is useful for transmitting a
CC signal to a variant receptor, which involves combining the variant
CC receptor with the ligand. The invention is useful for treating diseases
CC resulting due to variation receptor, such as type II diabetes and laron
CC syndrome. The ligand enables signal transduction function of
CC thrombopoietin, with respect to variant receptor. The present sequence is
CC used in the exemplification of the invention.
XX
SQ Sequence 255 AA;
Query Match 77.3%; Score 569.5; DB 8; Length 255;
Best Local Similarity 79.4%; Pred. No. 5e-45;
Matches 108; Conservative 9; Mismatches 14; Indels 5; Gaps 1;
Qy 1 MRVLILLWLTAFPGILSDVQLQESGPGLVKPSQSLTCSVTGYSTSGYAWNWIRQFP 60
Db 1 MRVLIPWLFTAFPGTLDVQLQESGPGLVKPSQSLTCTVTGYSTSDYAWNWIRQLP 60
Qy 61 GNKLEWNGYISYSGFTSYNPSLSRISFTRDTSKNQFFLQNLNSVTSEDTATYYCARWDYG 120
Db 61 GNKLEWNGYISYSGYIYNPSLSKRSISRTDTSKNQFLQNLNSVTEDTATYYCV----- 115
Qy 121 TTYGYFDVWGGQTTVT 136
Db 116 GGYDNMDYWGQTSVT 131
RESULT 10
ID ADS14288 standard; protein; 519 AA.
XX
AC ADS14288;
XX
DT 16-DEC-2004 (first entry)
XX
DE Murine protein relating to the invention SEQ ID NO:14.
XX variant receptor; antidiabetic; haemostatic; endocrine; thrombocytopenia;
KW type II diabetes; laron syndrome; thrombopoietin.
XX
OS Mus musculus.
XX
PN WO2004081048-A1.
XX

PD 23-SEP-2004.
XX
PF 12-MAR-2004; 2004WO-JP003334.
XX
PR 13-MAR-2003; 2003JP-00067832.
XX
PA (CHUS) CHUGAI SEIYAKU KK.
XX
PI Tsuchiya M, Hirata Y;
XX
DR WPI; 2004-677525/66.
DR N-PSDB; ADS14287.
XX
PT Novel ligand having agonist activity with respect to variant receptor
PT e.g.; variant thrombopoietin receptor, useful for treating disease
PT resulting due to variant receptor such as congenital non-megakaryocyte
PT thrombocytopenia.
XX
PS Disclosure; SEQ ID NO 14; 132pp; Japanese.
XX
CC The invention relates to a novel ligand (preferably an antibody) (I)
CC having agonist activity with respect to a variant receptor. A ligand of
CC the invention has antidiabetic, haemostatic and endocrine-gen. activity.
CC The ligand is useful for treating the disease caused due to variant
CC receptor, which involves combining the ligand/antibody with the variant
CC receptor, where the disease is congenital non-megakaryocyte
CC thrombocytopenia. A ligand of the invention is useful for transmitting a
CC signal to a variant receptor, which involves combining the variant
CC receptor with the ligand. The invention is useful for treating diseases
CC resulting due to variation receptor, such as type II diabetes and laron
CC syndrome. The ligand enables signal transduction function of
CC thrombopoietin, with respect to variant receptor. The present sequence is
CC used in the exemplification of the invention.
XX
SQ Sequence 519 AA;

Query Match 77.3%; Score 569.5; DB 8; Length 519;
Best Local Similarity 79.4%; Pred. No. 1.1e-44;
Matches 108; Conservative 9; Mismatches 14; Indels 5; Gaps 1;

QY 1 MRVLILLWLTAFPGILSDVQLQESGPGVLKPSQSLTCTVGYTSITSGYAWNWIRQPP 60
DB 1 MRVLPLWLTAFPGTLDVQLQESGPGVLKPSQSLTCTVGYTSITSDYAWNWIRQLP 60

QY 61 GNKLEWMIYISGFTSNPSLRISFTRDTSKNQFFLQNSVTSEDATYYCARWDYG 120
DB 61 GNKLEWMIYISGFTSNPSLRISFTRDTSKNQFFLQNSVTSEDATYYCV----- 115

QY 121 TTYGFDVWGQGTVT 136
DB 116 GGYNDNDYWGQGTSVT 131

RESULT 11
ADO44274
ID ADO44274 standard; protein; 120 AA.
XX
AC ADO44274;
XX
DT 15-JUL-2004 (first entry)
XX
DE Consensus sequence of variable heavy chain region of anti-C3-2.
XX
KW antibody; anti-C3-2; C3; C3a; C5a; complement activation;
KW inflammatory disease; kappa light chain.
XX
OS Mus sp.
XX
PN WO2004031240-A1.
XX
PD 15-APR-2004.
XX
PF 03-OCT-2003; 2003WO-EP010989.
XX
PI De Winter H, Buysse M, Hack E;

XX 04-OCT-2002; 2002EP-00447190.
PR 16-OCT-2002; 2002US-0418947P.
XX
XX (INNO-) INNOGENETICS NV.
PA (SANQ-) SANQUIN BLOOD SUPPLY FOUND AMSTERDAM.
XX
PI De Winter H, Buysse M, Hack E;
XX
DR WPI; 2004-316465/29.
XX
PT New molecule capable of inhibiting complement activation, and which
PT specifically binds on a functional domain exposed on native human C3,
PT useful for preventing or treating inflammatory diseases mediated by
PT activation of complement.
XX
XX Example 12; Fig 17; 72pp; English.
XX
CC The specification describes a monoclonal antibody, designated anti-C3-2,
CC which specifically binds on a functional domain exposed on native human
CC C3, thus inhibiting the generation of the biologically active peptides
CC such as C3a and C5a. The functional domain is in part located on the 23
CC kD-a-chain fragment of C3c. The antibody is useful for the preparation of
CC a medicament for inhibiting complement activation, preferably for
CC preventing or treating inflammatory diseases mediated by activation of
CC complement. The present sequence represents the consensus sequence of the
CC heavy chain variable region of the monoclonal antibody anti-C3-2, derived
CC from N-terminal sequencing, primer-induced sequence and sequence
CC confirmed by nested PCR.
XX
SQ Sequence 120 AA;

Query Match 75.5%; Score 556.5; DB 8; Length 120;
Best Local Similarity 89.0%; Pred. No. 3.5e-44;
Matches 105; Conservative 3; Mismatches 9; Indels 1; Gaps 1;

QY 19 DVQLQESGPGVLKPSQSLTCTVGYTSITSGYAWNWIRQPPGNKLEWMIYISGFTSY 78
DB 1 DVQLQESGPGVLKPSQSLTCTVGYTSITSDYAWNWIRQPPGNKLEWMIYISGFTSY 60

QY 79 NPSLRISFTRDTSKNQFFLQNSVTSEDATYYCARWDYGTYYGFDVWGQGTVT 136
DB 61 NPSLRISFTRDTSKNQFFLQNSVTSEDATYYCAR--DYDGAYWYFDVWGAGTIVT 117

RESULT 12
ADO44271
ID ADO44271 standard; protein; 120 AA.
XX
AC ADO44271;
XX
DT 15-JUL-2004 (first entry)
XX
DE Sequence of variable heavy chain region of the anti-C3-2 antibody.
XX
KW antibody; anti-C3-2; C3; C3a; C5a; complement activation;
KW inflammatory disease; kappa light chain.
XX
OS Mus sp.
XX
PN WO2004031240-A1.
XX
PD 15-APR-2004.
XX
PF 03-OCT-2003; 2003WO-EP010989.
XX
PR 04-OCT-2002; 2002EP-00447190.
PR 16-OCT-2002; 2002US-0418947P.
XX
XX (INNO-) INNOGENETICS NV.
PA (SANQ-) SANQUIN BLOOD SUPPLY FOUND AMSTERDAM.
XX
PI De Winter H, Buysse M, Hack E;

XX WPI; 2004-316465/29.
DR N-PSDB; ADO44270.
XX
PT New molecule capable of inhibiting complement activation, and which
PT specifically binds on a functional domain exposed on native human C3,
PT useful for preventing or treating inflammatory diseases mediated by
PT activation of complement.
XX
PS Disclosure; Fig 14B; 72pp; English.
XX
CC The specification describes a monoclonal antibody, designated anti-C3-2,
CC which specifically binds on a functional domain exposed on native human
CC C3, thus inhibiting the generation of the biologically active peptides
CC such as C3a and C5a. The functional domain is in part located on the 23
CC kD-a-chain fragment of C3c. The antibody is useful for the preparation of
CC a medicament for inhibiting complement activation, preferably for
CC preventing or treating inflammatory diseases mediated by activation of
CC complement. The present sequence represents the heavy chain region of the
CC monoclonal antibody anti-C3-2.
XX
SQ Sequence 120 AA;
Query Match 75.5%; Score 556.5; DB 8; Length 120;
Best Local Similarity 89.0%; Pred. No. 3.5e-44;
Matches 105; Conservative 3; Mismatches 9; Indels 1; Gaps 1;
QY 19 DVQLQESGFLVKPSQSLTCSVTGYSITSGYAWNWIRQFPNGKLEWVGYSYSGFTSY 78
DB 1 DVQLQESGFLVKPSQSLTCSVTGYSITSGYAWNWIRQFPNGKLEWVGYSYSGFTSY 60
QY 79 NPSLRSISFTSDTSKNQFFLQLNSVTSEDATYYCARWDYGTYYGVDFVWGQTTVT 136
DB 61 NPSLRSISFTSDTSKNQFFLQLNSVTSEDATYYCARWDYGTYYGVDFVWGQTTVT 117
RESULT 13
ADJ76886
ID ADJ76886 standard; protein; 127 AA.
XX
AC ADJ76886;
XX
DT 06-MAY-2004 (first entry)
XX
DE Anti-IGF-1R related protein #4.
XX
KW cytostatic; antipsoriatic; antibody;
KW insulin-like growth factor-1 receptor; IGF-1R; tyrosine kinase activity;
KW or epidermal growth factor receptor; EGFR; signal transduction pathway;
KW ligand; tumor; cancer; osteosarcoma; complementarity determining region;
KW CDR.
XX
OS Mus musculus.
XX
FN WO2003059951-A2.
XX
PD 24-JUL-2003.
XX
PF 20-JAN-2003; 2003WO-FR000178.
XX
PR 18-JAN-2002; 2002FR-00000653.
PR 18-JAN-2002; 2002FR-00000654.
PR 07-MAY-2002; 2002FR-00005753.
XX
XX (FABR) FABRE MEDICAMENT SA PIERRE.
XX
XX Goetsch L, Corvaia N, Leger O;
XX WPI; 2003-569653/53.
XX
XX New antibodies that bind to human insulin-like growth factor receptor,
XX useful for treatment, prevention and diagnosis of cancers.
XX

PS Disclosure; SEQ ID NO 52; 164pp; French.
XX
CC The invention relates to an isolated antibody (Ab), and its functional
CC fragments, that bind to human insulin-like growth factor-1 receptor (IGF-
CC 1R) and optionally: (i) inhibit natural binding of insulin-like growth
CC factors (IGF)-1 and/or -2; and/or (ii) inhibit specifically tyrosine
CC kinase activity of IGF-1R. Ab and its fragments are used to prevent or
CC treat diseases associated with overexpression and/or abnormal activity of
CC IGF-1R and/or epidermal growth factor receptor (EGFR) and/or with
CC hyperactivity of signal transduction pathways mediated by interaction of
CC these receptors with their ligands. Especially they inhibit
CC proliferation of tumor cells, so are useful against cancers of the
CC prostate, lung, breast, endometrium and colon, also osteosarcoma, and
CC also for treating psoriasis. Ab are also used to diagnose diseases caused
CC by abnormal expression of IGF-1R and/or EGFR. This sequence represents a
CC protein sequence used to generate the Ab of the invention.
XX
SQ Sequence 127 AA;
Query Match 75.2%; Score 554; DB 7; Length 127;
Best Local Similarity 82.0%; Pred. No. 6.5e-44;
Matches 105; Conservative 6; Mismatches 13; Indels 4; Gaps 2;
QY 9 LFTAFPGILSDVQLQESGFLVKPSQSLTCSVTGYSITSGYAWNWIRQFPNGKLEWVG 68
DB 1 LFTAFPGILSDVQLQESGFLVKPSQSLTCSVTGYSITSGYAWNWIRQFPNGKLEWVG 60
QY 69 YISYSGFTSYNPSLRSISFTSDTSKNQFFLQLNSVTSEDATYYCARWDYGTYYGVDFV 128
DB 61 YISYSGFTSYNPSLRSISFTSDTSKNQFFLQLNSVTSEDATYYCARWDYGTYYGVDFV 116
QY 129 WGOQTGTTT 136
DB 117 WGOQTGTTT 124
RESULT 14
ADZ67056
ID ADZ67056 standard; protein; 127 AA.
XX
AC ADZ67056;
XX
DT 30-JUN-2005 (first entry)
XX
DE Murine immunoglobulin heavy chain variable region 7C10 VH SEQ ID NO:52.
XX
KW Insulin-like growth factor 1 receptor; antibody; tumor; cytostatic;
KW neoplasm; prostate tumor; andrology; genitourinary disease; osteosarcoma;
KW musculoskeletal disease; respiratory disease; lung tumor;
KW endocrine disease; gynecology and obstetrics; breast tumor;
KW endometroid carcinoma; gastrointestinal disease; colon tumor;
KW antipsoriatic; psoriasis; dermatological disease; immune disorder;
KW immunoglobulin; heavy chain variable region.
XX
OS Mus musculus.
XX
XX
XX Key Location/Qualifiers
XX Peptide 1..10
XX /note= "leader peptide"
XX Region 41..46
XX /note= "CDR1"
XX Region 61..76
XX /note= "CDR2"
XX Region 109..116
XX /note= "CDR3"
XX
XX US2005084906-A1.
XX
XX 21-APR-2005.
XX
XX 16-DEC-2003; 2003US-00735916.
XX

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On protein - protein search, using sw model

Run on: May 19, 2006, 17:40:37 ; Search time 25.9048 Seconds
(without alignments)
505.138 Million cell updates/sec

Title: US-09-889-936A-6
Perfect score: 737
Sequence: 1 MRVLLILLMLFTAPPGILSDV.....WDYGTYYGYFDVWGQGTIVT 136

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues
Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : PIR80.*
1: pir1.*
2: pir2.*
3: pir3.*
4: pir4.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	605.5	82.2	135	2 PL0100	Ig heavy chain pre
2	587.5	79.7	134	2 B24672	Ig heavy chain pre
3	579	78.6	149	2 S30752	Ig heavy chain pre
4	561	76.1	137	1 AVMS35	Ig heavy chain pre
5	557	75.6	116	1 HVMS1B	Ig heavy chain v r
6	555.5	75.4	136	2 S07637	Ig heavy chain v r
7	539	73.1	116	1 HVMS31	Ig heavy chain pre
8	525.5	71.3	116	2 S38718	Ig heavy chain v r
9	524	71.1	121	2 S37200	Ig heavy chain v r
10	522	70.8	117	2 I28195	Ig heavy chain v r
11	509	69.1	119	2 C53285	Ig heavy chain v a
12	508.5	69.0	114	2 T01262	Ig heavy chain v r
13	504	68.4	119	2 E25114	Ig heavy chain v r
14	498.5	67.6	115	2 D33932	Ig mu chain precu
15	494	67.0	115	2 F25114	Ig heavy chain v r
16	487	66.1	119	2 C25114	Ig heavy chain v r
17	484.5	65.7	120	2 A25114	Ig heavy chain v r
18	476.5	64.7	117	1 HVMS73	Ig heavy chain pre
19	469	63.6	123	2 S42771	Ig heavy chain - m
20	466	63.2	106	2 S59639	Ig heavy chain v r
21	464.5	63.0	100	2 S14485	Ig heavy chain v r
22	463	62.8	119	2 D25114	Ig heavy chain v r
23	462.5	62.8	106	2 S26464	Ig heavy chain v r
24	461	62.6	117	2 I57810	gene C72-3A1 prote
25	455.5	61.8	104	2 S26467	Ig heavy chain v r
26	451	61.2	113	1 G2MS60	Ig heavy chain v r
27	441.5	59.9	102	2 S14488	Ig heavy chain v r
28	437	59.3	111	2 S13687	Ig heavy chain v r
29	437	59.3	140	2 I37782	Ig variable region

30	436.5	59.2	101	2 S14484	Ig heavy chain v r
31	435	59.0	112	2 S13685	Ig heavy chain v r
32	432	58.6	112	2 S13686	Ig heavy chain v r
33	427.5	58.0	102	2 S14487	Ig heavy chain v r
34	427	57.9	102	2 S14486	Ig heavy chain v r
35	426	57.8	110	2 S13688	Ig heavy chain v r
36	417	56.6	130	2 S31690	Ig heavy chain v r
37	416	56.4	123	2 S30530	Ig heavy chain - h
38	415.5	56.4	155	2 S31511	Ig heavy chain - h
39	414.5	56.2	94	2 S26461	Ig heavy chain v r
40	411.5	55.8	139	2 S31586	Ig heavy chain - h
41	409.5	55.6	155	2 S31512	Ig heavy chain v r
42	406	55.1	146	2 S09711	Ig heavy chain v r
43	402.5	54.6	137	2 S31676	Ig heavy chain v r
44	400	54.3	147	2 S13519	Ig heavy chain v r
45	397.5	53.9	145	2 S78055	Ig heavy chain pre

ALIGNMENTS

RESULT 1
PL0100
Ig heavy chain precursor V region (40-140) - mouse
C:Species: Mus musculus (house mouse)
C:Date: 07-Jun-1990 #sequence_revision 07-Jun-1990 #text_change 23-Jul-1999
C:Accession: PL0100
R:Near, R.I.; Haber, E.
Mol. Immunol. 26, 371-382, 1989
A:Title: Characterization of the heavy and light chain immunoglobulin variable region ger
A:Reference number: PL0100; MUID:89238344; PMID:2497340
A:Accession: PL0100
A:Molecule type: DNA
A:Residues: 1-135 <NEA>
A:Cross-references: UNIPARC:UPI0000114EA6; GB:M27660; NID:G341745; PIDN:AAA58746.1; PID:5
A:Experimental source: strain A/J
A:Note: the VH40-140 gene segment is classified as a member of the 36-60 VH gene family
C:Genetics:
A:Introns: 15/1
C:Superfamily: immunoglobulin V region; immunoglobulin homology
C:Keywords: heterotetramer; immunoglobulin
F:1-18/Domain: signal sequence #status predicted <SIG>
F:19-115/Domain: V segment #status predicted <VRE>
F:33-116/Domain: immunoglobulin homology <IMM>
F:117-118/Domain: D segment #status predicted <DRE>
F:119-135/Domain: J segment #status predicted <JRE>

Query Match 82.2%; Score 605.5; DB 2; Length 135;
Best Local Similarity 82.4%; Pred. No. 2.6e-45;
Matches 112; Conservative 12; Mismatches 7; Indels 5; Gaps 1;
QY 1 MRVLLILLMLFTAPPGILSDVQLQESGPGVLVKPSQSLTCSVTGYSITSGYAMNWIROFP 60
Db 1 MRVLLILLMLFTAPPGILSDVQLQESGPGVLVKPSQSLTCTVTGYSITSDYAMNWIROFP 60
QY 61 GNKLEWMGYISGFTSYNPSLRISRTDRTSKNQFFLQLNSVTSSEDTATYYCARWDYG 120
Db 61 GNRLEWMGYITNGYTYNPSLKRFSITRDTSKNQLFLQLSSVTTEDTATYYCAR---- 116
QY 121 TTYGYFDVWGQGTIVT 136
Db 117 -SYDYFDVWGQGTIVT 131

RESULT 2
B24672
Ig heavy chain precursor V region (VCAM3-2) - mouse
C:Species: Mus musculus (house mouse)
C:Date: 19-Nov-1988 #sequence_revision 19-Nov-1988 #text_change 18-Oct-1996
C:Accession: B24672
R:Winter, E.; Radbruch, A.; Krawinkel, U.
EMBO J. 4, 2861-2867, 1985
A:Reference number: A91022; MUID:86055722; PMID:2998759

S37200
Ig heavy chain V region - mouse
C:Species: Mus musculus (house mouse)
C:Date: 19-Mar-1997 #sequence_revision 19-Mar-1997 #text_change 21-Jan-2000
C:Accession: S37200
R:Fischer, R.; Voss, A.; Hunziker, W.; Stierhof, Y.D.; Kreuzaler, F.
submitted to the EMBL Data Library, August 1993
A:Description: Production and cloning of TMV-specific monoclonal antibodies.
A:Reference number: S37200
A:Accession: S37200
A:Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-121 <F1>
A:Cross-references: UNIPARC:UPI00001161AC; EMBL:X74587; NID:g402639; PID:g402640
C:Superfamily: immunoglobulin V region; immunoglobulin homology
F:15-98/Domain: immunoglobulin homology <IMM>

Query Match 71.1%; Score 524; DB 2; Length 121;
Best Local Similarity 82.6%; Pred. No. 2.4e-38;
Matches 100; Conservative 5; Mismatches 10; Indels 6; Gaps 2;

QY 19 DVQLQSGPGLVKPSQSLTCSVTGYSTSGYAWNWIRQFPGNKLEWMGYISYSGFTSY 78
DB 1 DVQLQSGPGLVKPSQSLTCSVTGYSTSGYAWNWIRQFPGNKLEWMGYISYDGRNDY 60
QY 79 NPSLRISRIFTRTSKNQFPLQLNSVTSEDTATYTCARWDYGTYYG---YFDVWGQGTTV 135
DB 61 NPSLKNRISITRDTSKNQFPLKLSNVTEDTATYYCAR---GGIYGDDYFDSWGQGTTL 117
QY 136 T 136
DB 118 T 118

RESULT 10
I28195
Ig heavy chain V region (anti-haloperidol antibody D) - mouse
C:Species: Mus musculus (house mouse)
C:Date: 01-Dec-1989 #sequence_revision 30-Sep-1991 #text_change 23-Jul-1999
C:Accession: I28195
R:Sherman, M.A.; Deans, R.J.; Bolger, M.B.
J. Biol. Chem. 263, 4059-4063, 1988
A:Title: Haloperidol binding to monoclonal antibodies. Hypervariable region amino acid
A:Reference number: A28195; MUID:88153717; PMID:3267217
A:Accession: I28195
A:Molecule type: mRNA
A:Residues: 1-117 <SHE>
A:Cross-references: UNIPARC:UPI0000114D72; GB:M19775; NID:g195526; PIDN:AAA38343.1; PID:
A:Note: the authors translated the codon AAC for residue 61 as Thr, and did not translate
C:Superfamily: immunoglobulin V region; immunoglobulin homology
C:Keywords: heterotrimer; immunoglobulin
F:15-98/Domain: immunoglobulin homology <IMM>

Query Match 70.8%; Score 522; DB 2; Length 117;
Best Local Similarity 85.6%; Pred. No. 3.4e-38;
Matches 101; Conservative 5; Mismatches 8; Indels 4; Gaps 2;

QY 19 DVQLQSGPGLVKPSQSLTCSVTGYSTSGYAWNWIRQFPGNKLEWMGYISYSGFTSY 78
DB 1 DVQLQSGPGLVKPSQSLTCTVTGYSTSEYAWNWIRQFPGNKLEWMGYISYSGTTSY 60
QY 79 NPSLRISRIFTRTSKNQFPLQLNSVTSEDTATYTCARWDYGTYYGFDVWGQGTTVT 136
DB 61 NPSLKNRISITRDTSKNQFPLQLNSVTEDTATYYCAR--DNGNCGDY--WGQGTSTV 114

REDACTED 11
C55
Ig heavy chain V and J regions, monoclonal antibody OHP7D7.2.3 - mouse (fragment)
C:Species: Mus musculus (house mouse)
C:Date: 02-May-1994 #sequence_revision 18-Nov-1994 #text_change 20-Jun-2000
C:Accession: C53285
R:Sawada, J.; Mizusawa, S.; Terao, T.; Naito, M.; Kurosawa, Y.

C:Keywords: heterotetramer; immunoglobulin
F:15-98/Domain: immunoglobulin homology <IMM>
Query Match 68.4%; Score 504; DB 2; Length 119;
Best Local Similarity 81.5%; Pred. No. 1-2e-36;
Matches 97; Conservative 5; Mismatches 13; Indels 4; Gaps 2;
QY 19 DVQLQESGGLVKPSQSLTSCVTGYSTGYANNWIRQFGKLEWMGYISYSGFTSY 78
DB 1 DVQLQESGGLVKPSQSLTSCVTGYSTGYANNWIRQFGKLEWMGYISYSGSHNY 60
QY 79 NPSLSRISFTSDTSKNQFFLOLNSVTSSEDTATYYCAR--WDYGTGYG-FDVMGQGT 133
DB 61 NPSLKNRISITRDTSKNQFFLNSVTIEDTATYYCARPLYRYRYDEYYAMDYWGQGT 119
RESULT 14
D33932
Ig mu chain precursor V region (E7) - mouse
C:Species: Mus musculus (house mouse)
C:Date: 09-Mar-1990 #sequence_revision 09-Mar-1990 #text_change 23-May-1997
C:Accession: D33932
R:Baccala, R.; Vo Quang, T.; Gilbert, M.; Ternynck, T.; Avrameas, S.
Proc. Natl. Acad. Sci. U.S.A. 86, 4624-4628, 1989
A:Title: Two murine natural polyreactive autoantibodies are encoded by nonmutated germ-
A:Reference number: A33932; MUID:89282823; PMID:2499887
A:Accession: D33932
A:Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-115 <BAC>
A:Cross-references: UNIPARC:UPI00001768F1; GB:M27106
C:Superfamily: immunoglobulin V region; immunoglobulin homology
C:Keywords: immunoglobulin
F:33-115/Domain: immunoglobulin homology <IMM>
Query Match 67.6%; Score 498.5; DB 2; Length 115;
Best Local Similarity 83.6%; Pred. No. 3.5e-36;
Matches 97; Conservative 9; Mismatches 9; Indels 1; Gaps 1;
QY 1 MRVILLMLFTAPPGLSDVQLQESGGLVKPSQSLTSCVTGYSTGYANNWIRQFP 60
DB 1 MVLVLLYLTALPGLSEVQLQESGGLVKPSQSLTSCVTGDSITSGY-WNWRKFP 59
QY 61 GNKLEWMGYISYSGFTSYNPSLSRISFTSDTSKNQFFLOLNSVTSSEDTATYYCAR 116
DB 60 GNKLEWMGYISYSGFTSYNPSLSRISFTSDTSKNQFFLOLNSVTSSEDTATYYCAR 115
RESULT 15
F25114
Ig heavy chain V region (HP12) - mouse
C:Species: Mus musculus (house mouse)
C:Date: 29-Aug-1987 #sequence_revision 29-Aug-1987 #text_change 20-Jun-2000
C:Accession: F25114
R:Ollier, P.; Rocca-Serra, J.; Somme, G.; Theze, J.; Fougereau, M.
EMBO J. 4, 3681-3688, 1985
A:Title: The idiotypic network and the internal image: possible regulation of a germ-
A:Reference number: A91028; MUID:86136012; PMID:3937730
A:Accession: F25114
A:Molecule type: mRNA
A:Residues: 1-115 <OLL>
A:Cross-references: UNIPARC:UPI0000115D28; GB:X03379; NID:g52013; PIDN:CAA27101.1; PID:g
C:Superfamily: immunoglobulin V region; immunoglobulin homology
C:Keywords: heterotetramer; immunoglobulin
F:15-98/Domain: immunoglobulin homology <IMM>
Query Match 67.0%; Score 494; DB 2; Length 115;
Best Local Similarity 79.1%; Pred. No. 8.6e-36;
Matches 91; Conservative 8; Mismatches 16; Indels 0; Gaps 0;
QY 19 DVQLQESGGLVKPSQSLTSCVTGYSTGYANNWIRQFGKLEWMGYISYSGFTSY 78
DB 1 DVQLQESGGLVKPSQSLTSCVTGYSTGYANNWIRQFGKLEWMGYIRYDGSNNY 60

QY 79 NPSLSRISFTSDTSKNQFFLOLNSVTSSEDTATYYCARWDYGTGYFDVMGQGT 133
DB 61 NPSLKNRISITRDTSKNQFFLNSVTIEDTATYYCAVFGYDMDYYAMDYWGQGT 115

Search completed: May 19, 2006, 17:47:23
Job time : 26.9048 secs



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ORF-protein - protein search, using sw model

Run on: May 19, 2006, 17:34:57 ; Search time 207.238 Seconds
(without alignments)
607.041 Million cell updates/sec

Title: US-09-889-936A-6
Perfect score: 737
Sequence: 1 MRVLLMLWLTAPPGILSDV.....WDYGTGYFDVWGQGTIVT 136

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 2849598 seqs, 92501592 residues

Total number of hits satisfying chosen parameters: 2849598

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : UniProt 7.2.*
1: uniprot_sprot.*
2: uniprot_trembl.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Match	Query %	Length	ID	Description
1	609.5	82.7	483	2	Q5U413_MOUSE	Q5U413 mus musculus
2	568	77.1	479	2	Q9NM22_MOUSE	Q9NM22 mus musculus
3	561	76.1	137	1	HV46_MOUSE	P01822 mus musculus
4	561	76.1	615	2	Q569B6_RAT	Q569b6 rattus norv
5	557	75.6	116	1	HV61_MOUSE	P18532 mus musculus
6	555.5	75.4	136	2	Q6L8Q5_MOUSE	Q6L8q5 mus musculus
7	548	74.4	590	2	Q569B8_RAT	Q569b8 rattus norv
8	539	73.1	116	1	HV60_MOUSE	P18531 mus musculus
9	504	68.4	119	2	Q53VQ5_MOUSE	Q53vg5 mus musculus
10	494	67.0	115	2	Q53VQ1_MOUSE	Q53vg1 mus musculus
11	487	66.1	119	2	Q53VR3_MOUSE	Q53vr3 mus musculus
12	484.5	65.7	120	2	Q53VR7_MOUSE	Q53vr7 mus musculus
13	476.5	64.7	117	1	HV62_MOUSE	P18533 mus musculus
14	473	64.2	98	2	Q53VQ4_MOUSE	Q53vg4 mus musculus
15	463	62.8	119	2	Q53VQ2_MOUSE	Q53vg2 mus musculus
16	462	62.7	98	2	Q53VR2_MOUSE	Q53vr2 mus musculus
17	458	62.1	98	2	Q53VR6_MOUSE	Q53vr6 mus musculus
18	453	61.5	98	2	Q53VQ0_MOUSE	Q53vg0 mus musculus
19	451	61.2	113	1	HV47_MOUSE	P01823 mus musculus
20	450	61.1	262	2	Q65Z11_MOUSE	Q65z11 mus musculus
21	443	60.1	98	2	Q53VQ8_MOUSE	Q53vg8 mus musculus
22	428.5	58.1	478	2	Q72379_HUMAN	Q72379 homo sapien
23	423.5	57.5	477	2	Q6GNX7_HUMAN	Q6gnx7 homo sapien
24	420	57.0	476	2	Q6GNX1_HUMAN	Q6gnx1 homo sapien
25	403.5	54.7	465	2	Q6GNX6_HUMAN	Q6gnx6 homo sapien
26	399.5	54.2	576	2	Q6PA18_HUMAN	Q6pa18 homo sapien
27	397.5	53.9	477	2	Q51OJ1_RAT	Q51oj1 rattus norv
28	395	53.6	591	2	Q51OL9_RAT	Q51ol9 rattus norv
29	392.5	53.3	144	1	HV43_MOUSE	P01819 mus musculus
30	392	53.2	478	2	Q6NTH3_HUMAN	Q6nth3 homo sapien
31	389.5	52.8	469	2	Q5M839_RAT	Q5m839 rattus norv

32	387	52.5	119	2	Q9UL73_HUMAN	Q9ul73 homo sapien
33	386.5	52.4	146	1	HV21_HUMAN	P06331 homo sapien
34	386.5	52.4	458	2	Q5M842_RAT	Q5m842 rattus norv
35	382.5	51.9	492	2	Q72374_HUMAN	Q72374 homo sapien
36	382	51.8	139	2	Q86SX2_HUMAN	Q86sx2 homo sapien
37	381.5	51.8	620	2	Q96EY0_HUMAN	Q96ey0 homo sapien
38	374.5	50.8	496	2	Q96KX8_HUMAN	Q96kx8 homo sapien
39	372.5	50.5	150	2	Q95973_HUMAN	Q95973 homo sapien
40	370	50.2	597	2	Q9BQB8_HUMAN	Q9bqb8 homo sapien
41	369	50.1	482	2	Q91X92_MOUSE	Q91x92 mus musculus
42	368	49.9	595	2	Q8WUX4_HUMAN	Q8wux4 homo sapien
43	368	49.9	597	2	Q6GMX5_HUMAN	Q6gmx5 homo sapien
44	368	49.9	597	2	Q9BU10_HUMAN	Q9bu10 homo sapien
45	368	49.9	625	2	Q96AA6_HUMAN	Q96aa6 homo sapien

ALIGNMENTS

RESULT 1
Q5U413_MOUSE PRELIMINARY; PRT; 483 AA.
AC Q5U413-
DT 07-DEC-2004, integrated into UniProtKB/TrEMBL.
DT 07-DEC-2004, sequence version 1.
DE LOC544903 protein.
GN Name=LOC544903;
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
OC Murioidea; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=FVB/N; TISSUE=Colon;
RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Diachenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Donald M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Udwin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahey J., Helton E., Kettman M., Madan A., Rodriguez S., Sanchez A.,
RA Whitling M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
RA Butterfield Y.S.N., Krzywinaki M.I., Skaleka U., Smalhus D.E.,
RA Scherch A., Schein J.E., Jones S.J.M., Marra M.A.,
RT "Generation and initial analysis of more than 15,000 full-length human
and mouse cDNA sequences.";
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903 (2002).
RN [2]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=FVB/N; TISSUE=Colon;
RG NIH MGC Project;
RL Submitted (OCT-2004) to the EMBL/GenBank/DBJ databases.
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CC -----
CC EMBL; BC085312; AAH85312.1; -; mRNA.
CC Ensembl; ENSMUSG0000054328; Mus musculus.
DR InterPro; IPR003599; IG.
DR InterPro; IPR007110; IG-like.
DR InterPro; IPR003597; IG-cl.
DR InterPro; IPR003006; IG_MHC.
DR InterPro; IPR003596; IG_v.

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DR InterPro; IPR013106; V-set.
DR Pfam; PF07654; Cl-set; 2.
DR SMART; SM00409; IG; 2.
DR SMART; SM00407; IGcl; 2.
DR SMART; SM00406; IGv; 1.
DR PROSITE; PS00359; IG LIKE; 4.
DR PROSITE; PS00290; IG MHC; UNKNOWN 2.
SQ SEQUENCE 483 AA; 52714 MW; 7C272DA501A4A0D1 CRC64;

Query Match      82.7%; Score 609.5; DB 2; Length 483;
Best Local Similarity 85.4%; Pred. No. 2.4e-50;
Matches 117; Conservative 6; Mismatches 11; Indels 3; Gaps 2;

QY 1 MRVLLLLWLTAFPGILSDVQLQESGPGVLKPSQSLTCSVTGYTSITSGYAWNWIRQFP 60
DB 1 MRVLLLLWLTAFPGILSDVQLQESGPGDLKPSQSLTCTVGTGYTSITSGYAWNWIRQFP 60
QY 61 GNKLEWMGYISYSGFTSYNPSLRISIFTRDTSKNQFFLQLNSVTSEDTATYYCARWDYG 120
DB 61 GNKLEWMGYISYSGFTSYNPSLRISITRDTSKNQFFLQLNSVTSEDTATYYCAR--YE 118
QY 121 TTYGY-FDVWGQGTVT 136
DB 119 GNYDYAMDYWGQGTSTV 135

RESULT 2
Q95M22_MOUSE
ID AC Q95M22_MOUSE PRELIMINARY; PRT; 479 AA.
DT 01-JUN-2001, integrated into UniProtKB/TrEMBL.
DT 07-FEB-2006, entry version 31.
DE LOC238447 protein.
GN Name=LOC238447;
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
OC Muridae; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
[1]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=Mix FVB/N; TISSUE=Mammary tumor. WAP-TGF alpha model. 7 months
old;
RX MEDLINE=22389257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA Klausner R.B., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.P., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Frange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahey J., Helton E., Kettner M., Madan A., Rodriguez S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
RA Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E.,
RA Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human
and mouse cDNA sequences.";
RJ Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903 (2002).
TN [2]
RF NUCLEOTIDE SEQUENCE.
RC STRAIN=Mix FVB/N; TISSUE=Mammary tumor. WAP-TGF alpha model. 7 months
old;
RG NIH MGC Project;
RL Submitted (JAN-2001) to the EMBL/GenBank/DBJ databases.
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CC -----
DR EMBL; BC002091; AA02091.1; -, mRNA.
DR HSRF; P01820; IG7J.
DR Ensembl; ENSMUSG00000054328; Mus musculus.
DR InterPro; IPR003599; IG.
DR InterPro; IPR007110; IG-like.
DR InterPro; IPR003597; IG cl.
DR InterPro; IPR003006; IG_MHC.
DR InterPro; IPR003596; IG_v.
DR InterPro; IPR013106; V-set.
DR Pfam; PF07654; Cl-set; 2.
DR SMART; SM00409; IG; 2.
DR SMART; SM00407; IGcl; 2.
DR SMART; SM00406; IGv; 1.
DR PROSITE; PS00359; IG LIKE; 4.
DR PROSITE; PS00290; IG MHC; UNKNOWN 2.
SQ SEQUENCE 479 AA; 51992 MW; 768E39A138918892 CRC64;

Query Match      77.1%; Score 568; DB 2; Length 479;
Best Local Similarity 79.4%; Pred. No. 2.5e-46;
Matches 108; Conservative 9; Mismatches 15; Indels 4; Gaps 1;

QY 1 MRVLLLLWLTAFPGILSDVQLQESGPGVLKPSQSLTCSVTGYTSITSGYAWNWIRQFP 60
DB 1 MKVLSLLVLLTAIPGILSDVQLQESGPGVLKPSQSLTCSVTGYTSITSGYAWNWIRQFP 60
QY 61 GNKLEWMGYISYSGFTSYNPSLRISIFTRDTSKNQFFLQLNSVTSEDTATYYCARWDYG 120
DB 61 GNKLEWMGYISYSGFTSYNPSLRISITRDTSKNQFFLQLNSVTSEDTATYYCA----S 116
QY 121 TTYGYFDVWGQGTVT 136
DB 117 RGSWFFPNWGQGTTLV 132

RESULT 3
HV46_MOUSE
ID HV46_MOUSE STANDARD; PRT; 137 AA.
AC P01822;
DT 21-JUL-1986, integrated into UniProtKB/Swiss-Prot.
DT 01-AUG-1992, sequence version 2.
DT 07-MAR-2006, entry version 51.
DE Ig heavy chain V region MOPC 315 precursor.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
OC Muridae; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
[1]
RP NUCLEOTIDE SEQUENCE (GENOMIC DNA).
RX MEDLINE=89238351; PubMed=2497341; DOI=10.1016/0161-5890(89)90133-8;
RA Rinfret A., Horne C., Dorrington K.J., Klein M.;
RT "Cloning, sequencing and expression of the rearranged MOPC 315 VH gene
segment.";
RL Mol. Immunol. 26:431-434 (1989).
[2]
RN [2]
RP PROTEIN SEQUENCE OF 1-31.
RX MEDLINE=78094475; PubMed=414225;
RA Jilka R.L., Pestka S.;
RT "Amino acid sequence of the precursor region of MOPC-315 mouse
immunoglobulin heavy chain.";
RL Proc. Natl. Acad. Sci. U.S.A. 74:5692-5696 (1977).
[3]
RN [3]
RP PROTEIN SEQUENCE OF 1-21.
RX MEDLINE=79148758; PubMed=428562;
RA Schechter I., Wolf O., Zemell R., Burstein Y.;
RT "Structure and function of immunoglobulin genes and precursors.";
RL Fed. Proc. 38:1839-1845 (1979).
[4]
RN [4]
RP PROTEIN SEQUENCE OF 19-136.
RX MEDLINE=74170779; PubMed=4524622;
RA Francis S.H., Leslie R.G.Q., Hood L., Eisen H.N.;
```

RT- "Amino-acid sequence of the variable region of the heavy (alpha) chain
 of a mouse myeloma protein with anti-hapten activity.";
 RL P roc. Natl. Acad. Sci. U.S.A. 71:1123-1127(1974).
 RN [5]
 RP /SEQUENCE REVISION TO 53.
 RA MEDLINE=77244979; PubMed=268248;
 RA Padlan E.A., Davies D.R., Pecht I., Givol D., Wright C.;
 RT "Model-building studies of antigen-binding sites: the hapten-binding
 site of mOp-315.";
 RL Cold Spring Harb. Symp. Quant. Biol. 41:627-637(1977).
 CC -I- MISCELLANEOUS: This alpha chain was isolated from a myeloma
 protein that has anti-dinitrophenyl activity.
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 CC -----
 DR EMBL; M27638; AAA61337.1; -; Genomic DNA.
 DR EMBL; X07880; CAA30727.1; -; Genomic DNA.
 DR FIR; PLO102; AVMS35.
 DR HSP; P01822; IG7J.
 DR SMR; P01822; 20-137.
 DR Ensemble; ENSMUSG0000057048; Mus musculus.
 DR InterPro; IPR003599; Ig.
 DR InterPro; IPR007110; Ig-like.
 DR InterPro; IPR003596; Ig_v.
 DR InterPro; IPR013106; V-set.
 DR Pfam; PF07686; V-set; 1.
 DR SMART; SM00409; IG; 1.
 DR SMART; SM00406; IGv; 1.
 DR PROSITE; PS50835; IG_LIKE; 1.
 DR Direct protein sequencing; Immunoglobulin domain;
 KW Immunoglobulin V region; Signal.
 FT SIGNAL 1 18
 FT CHAIN 19 137
 FT Ig heavy chain V region MOPC 315.
 FT /STID-PRO 0000015232.
 FT Framework-1.
 FT REGION 19 48
 FT REGION 49 54
 FT Complementarity-determining-1.
 FT REGION 55 68
 FT Framework-2.
 FT REGION 69 84
 FT Complementarity-determining-2.
 FT REGION 85 116
 FT Framework-3.
 FT REGION 117 126
 FT Complementarity-determining-3.
 FT REGION 127 137
 FT Framework-4.
 FT DISULFID 40 114
 FT By similarity.
 FT CONFLICT 15 15 G -> GG (in Ref. 1; CAA30727).
 FT CONFLICT 15 15 G -> H (in Ref. 2).
 FT CONFLICT 77 78 GV -> YG (in Ref. 4).
 FT CONFLICT 102 102 N -> D (in Ref. 4).
 FT CONFLICT 123 123 Missing (in Ref. 4).
 FT NON_TER 137 137
 FT SEQUENCE 137 AA; 15399 MW; FB3828304C2B81DC CRC64;
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 Query Match 76.1%; Score 561; DB 1; Length 137;
 Best Local Similarity 77.9%; Pred. No. 3e-46;
 Matches 106; Conservative 12; Mismatches 16; Indels 2; Gaps 2;
 QY 1 MRVILLMLFTAPPGLSDVQLQESGPGLVKPSQSLSLTCSVTGYSITSGYAWNWIRQPP 60
 Db 1 MKVLSLLYLLTALPGIMSDVQLQESGPGLVKPSQSLSLTCSVTGYSITSGYFWNWIRQPP 60
 QY 61 GNKLEWMGYISYSGFTSYNPSLRISFTRDTSKNQFFLQNSVTSEDATYYCARWDYG 120
 Db 61 GNKLEWLGPIKYDGSNGYNPSLKNRVSITRDTSKNQFFLKLNSVTEDATYYCA-GDND 119
 QY 121 TTYG-YFDVWVGQGTVT 136
 Db 120 HLY-YFDVWVGQGTTLT 134
 RESULT 4
 Q569B6 RAT
 ID Q569B6_RAT PRELIMINARY; PRT; 615 AA.
 AC Q569B6;
 DT 10-MAY-2005, integrated into UniProtKB/TrEMBL.

DT 10-MAY-2005, sequence version 1.
 DT 07-FEB-2006, entry version 12.
 DE LOC314509 protein.
 GN Name=LOC314509;
 OS Rattus norvegicus (Rat).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
 OC Muridae; Muridae; Murinae; Rattus.
 OX NCBI_TaxID=10116;
 RN [1]
 RP NUCLEOTIDE SEQUENCE.
 RC TISSUE-Spleen.
 RX MEDLINE=2238857; PubMed=12477932; DOI=10.1073/pnas.242603899;
 RA Klausner R.L., Feingold E.A., Grouse L.H., Derge J.G.,
 RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
 RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
 RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
 RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
 RA Stapleton M., Soares M.B., Donald M.P., Casavant T.L., Scheetz T.E.,
 RA Brownstein M.J., Udén T.B., Toshiyuki S., Carninci P., Prange C.,
 RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mulláhy S.J.,
 RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
 RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
 RA Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
 RA Fahey J., Helton E., Kettelman M., Madan A., Rodrigues S., Sanchez A.,
 RA Whitling M., Madan A., Young A.C., Green E.D., Bouffard G.G.,
 RA Blakesley R.W., Touchman J.W., Shevchenko Y., Bouffard G.G.,
 RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
 RA Butterfield Y.S.N., Krzywicki M.I., Skalek U., Smailus D.E.,
 RA Scherch A., Schein J.E., Jones S.J.M., Marra M.A.,
 RT "Generation and initial analysis of more than 15,000 full-length human
 and mouse cDNA sequences.";
 RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
 RN [2]
 RP NUCLEOTIDE SEQUENCE.
 RC TISSUE-Spleen;
 RG NIH MGC Project;
 RL Submitted (APR-2005) to the EMBL/GenBank/DBJ databases.
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 CC -----
 CC EMBL; BC092582; AAH92582.1; -; mRNA.
 DR InterPro; IPR003599; Ig.
 DR InterPro; IPR007110; Ig-like.
 DR InterPro; IPR003597; Ig_c1.
 DR InterPro; IPR003006; Ig_MHC.
 DR InterPro; IPR003596; Ig_v.
 DR InterPro; IPR013106; V-set.
 DR Pfam; PF07654; C1-set; 4.
 DR SMART; SM00409; IG; 1.
 DR SMART; SM00406; IGv; 1.
 DR PROSITE; PS50835; IG_LIKE; 5.
 DR PROSITE; PS00290; IG_MHC; UNKNOWN 3.
 SQ SEQUENCE 615 AA; 67986 MW; BE5C2483C69F186C CRC64;
 Query Match 76.1%; Score 561; DB 2; Length 615;
 Best Local Similarity 80.3%; Pred. No. 1.6e-45;
 Matches 110; Conservative 8; Mismatches 17; Indels 2; Gaps 2;
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 Db 1 MRTLGLLYLLTALPGILSEVQLQESGPGLVKPSQSLSLTCSVTGYSITSGY-
 QY 61 GNKLEWMGYISYSGFTSYNPSLRISFTRDTSKNQFFLQNSVTSEDATYYCARWDYG 120
 Db 60 GNKMEWIGHISYSGTSYNPSLKRISITRDTSKNQFFLQNSVTEDATYYCARHGG 119
 QY 121 TTYG-YFDVWVGQGTVT 136
 Db 120 PLTGRFYDWVGQVWVT 136

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RESULT 5
HV61_MOUSE STANDARD; PRT; 116 AA.
AC P18532;
DT 01-NOV-1990, integrated into UniProtKB/Swiss-Prot.
DT 01-NOV-1990, sequence version 1.
DT 07-NAR-2006, entry version 44.
DE Ig heavy chain V region 1B43 precursor.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
OC Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]_
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=BALB/cJ;
RX MEDLINE=89279149; PubMed=2499654; DOI=10.1084/jem.169.6.2007;
RA Levy N.S., Malpiero U.V., Lebecque S.G., Gearhart P.J.;
RT "Early onset of somatic mutation in immunoglobulin VH genes during the
RT primary immune response.";
RL J. Exp. Med. 169:2007-2019(1989).
CC -!- MISCELLANEOUS: This sequence belongs to the VH3660 subfamily.
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PIR; J70509; HVMS1B.
DR PDB; 1KCS; X-ray; H=25-116.
DR PDB; 1KCV; X-ray; H=25-116.
DR Ensembl; ENSMUSG00000061612; Mus musculus.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003596; Ig_v.
DR InterPro; IPR013106; V-set.
DR Pfam; PF07686; V-set; 1.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PS50835; IG LIKE; 1.
KW 3D-structure; Immunoglobulin domain; Immunoglobulin V region; Signal.
FT SIGNAL 1 18
FT CHAIN 19 116
Ig heavy chain V region 1B43.
/FTID=PRO_0000015242.
Framework-1.
REGION 19 48
Complementarity-determining-1.
REGION 49 53
Framework-2.
REGION 54 67
Complementarity-determining-2.
REGION 68 84
Complementarity-determining-3.
REGION 85 116
Framework-3.
FT DISULFID 40 114
FT NON_TER 116 116
By similarity.
FT STRAND 21 25
FT STRAND 28 30
FT STRAND 32 33
FT TURN 34 34
FT STRAND 36 45
FT STRAND 47 49
FT STRAND 50 58
FT TURN 60 61
FT STRAND 64 71
FT TURN 72 73
FT STRAND 74 74
FT STRAND 76 78
FT TURN 80 85
FT STRAND 86 91
FT TURN 92 95
FT STRAND 96 101
FT STRAND 103 103
FT HELIX 106 108
FT STRAND 110 116
SEQUENCE 116 AA; 13158 MW; 1CB547253681FF74 CRC64;
Query Match 75.6%; Score 557; DB 1; Length 116;
Best Local Similarity 91.4%; Pred. No. 6.1e-46;
Matches 100; Conservative 5; Mismatches 5; Indels 0; Gaps 0;
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QY 1 MRVLILLWLTAFPGILSDVOLQESGPGLVKPSQSLTCSVTGYTSITGYAMNWIROP 60
Db 1 MRVLILLCLFTAFPGILSDVOLQESGPGDLVPSQSLTCTVTGYTSITGYAMNWIROP 60
QY 61 GNKLEWMGYISYSGFTSYNPSLSRISFTTRDTSKNQFFLQNLNSVTSEDTATYYCAR 116
Db 61 GNKLEWMGYIHYSGNTSYNPSLSRISFTTRDTSKNQFFLQNLNSVTSEDTATYYCAR 116
RESULT 6
Q6LBQ5_MOUSE PRELIMINARY; PRT; 136 AA.
AC Q6LBQ5;
DT 05-JUL-2004, integrated into UniProtKB/TrEMBL.
DT 05-JUL-2004, sequence version 1.
DT 07-FEB-2006, entry version 11.
DE VH gene product (Fragment).
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
OC Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]_
RP NUCLEOTIDE SEQUENCE.
RX MEDLINE=90067954; PubMed=2587273;
RA Urakov D.N., Deev S.M., Polyanovsky O.L.;
RT "The structure of the expressible VH gene from a hybridoma producing
RT monoclonal antibodies against porcine transferrin.";
RL Nucleic Acids Res. 17:9481-9481(1989).
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EMBL; X16740; CAA34714.1; -; Genomic_DNA.
DR HSSP; P18532; 1KCV.
DR SMR; Q6LBQ5; 20-136.
DR Ensembl; ENSMUSG00000057048; Mus musculus.
DR InterPro; IPR003599; Ig.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003596; Ig_v.
DR InterPro; IPR013106; V-set.
DR SMART; SM00409; IGV; 1.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PS50835; IG LIKE; 1.
KW Immunoglobulin domain.
KW NON_TER 1
SQ SEQUENCE 136 AA; 15307 MW; 5B0F439CCFB15C3A CRC64;
Query Match 75.4%; Score 555.5; DB 2; Length 136;
Best Local Similarity 77.9%; Pred. No. 1e-45;
Matches 106; Conservative 9; Mismatches 18; Indels 3; Gaps 1;
QY 1 MRVLILLWLTAFPGILSDVOLQESGPGLVKPSQSLTCSVTGYTSITGYAMNWIROP 60
Db 1 MKVLSLLVLTAFPGILSTVOLQESGPGLVKPSQSLTCSVTDFITSITGYAMNWIROP 60
QY 61 GNKLEWMGYISYSGFTSYNPSLSRISFTTRDTSKNQFFLQNLNSVTSEDTATYYCAR 120
Db 61 GNKLEWMGYISYSGFTSYNPSLSRISFTTRDTSKNQFFLQNLNSVTSEDTATYYCTR 117
QY 121 TTYGYFDVWGGTQTVT 136
Db 118 DGYHFFTYWGGTQTVT 133
RESULT 7
Q569B8_MOUSE PRELIMINARY; PRT; 590 AA.
AC Q569B8;
DT 10-MAY-2005, integrated into UniProtKB/TrEMBL.
DT 10-MAY-2005, sequence version 1.
DT 07-FEB-2006, entry version 13.
DE RGD1359202 protein.
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GN: Name=RGDI359202;
AS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
CC Muridae; Muridae; Murinae; Rattus.
OX NCBI_TaxID=10116;
RN [1].
RP NUCLEOTIDE SEQUENCE.
RC TISSUE=Spleen;
RX MEDLINE=22398257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA Srausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shennan C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Hsieh F.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Diatchenko L., Marasina K., Farmer A.A., Rubin G.M., Hong L.,
RA Scapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Uadin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullany S.J.,
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahey J., Helton E., Kettman M., Madan A., Rodriguez S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakeley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
RA Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smallos D.E.,
RA Schnarch A., Schein J.E., Jones S.J.M., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human
and mouse cDNA sequences";
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN [2].
RP NUCLEOTIDE SEQUENCE.
RC TISSUE=Spleen;
RG NIH MGC Project;
RL Submitted (APR-2005) to the EMBL/GenBank/DBJ databases.
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CC -----
CC EMBL: BC092580; AAH92580.1; -; mRNA.
DR InterPro: IPR003599; Ig.
DR InterPro: IPR007110; Ig-like.
DR InterPro: IPR003597; Ig.C1.
DR InterPro: IPR003006; Ig.MHC.
DR InterPro: IPR003596; Ig.V.
DR InterPro: IPR013106; V-set.
DR Pfam: PF07654; C1-set; 4.
DR SMART: SM00409; IG; 1.
DR SMART: SM00407; IGc1; 2.
DR SMART: SM00406; IG; 1.
DR PROSITE: PS00835; IG LIKE; 5.
DR PROSITE: PS00290; IG_MHC; UNKNOWN 3.
SQ SEQUENCE 590 AA; 55088 MW; FAC77FFA82302304 CRC64;

Query Match 74.4%; Score 548; DB 2; Length 590;
Best Local Similarity 78.4%; Pred. No. 2.7e-44;
Matches 105; Conservative 11; Mismatches 16; Indels 2; Gaps 1;

OY 3 VLILLWLFAPGILSDVQLQESGPGLVKPSQSLTCSVTGYSTSGYANNWIROP 62
DB 1 MLVLLYLLTALPGILSEVQLQESGPGLVKPSQSLTCSVTGYSTSGYANNWIROP 60

OY 63 KLEWMGYISYSGFTSYNPSLRISIFTRDTSKNQFFLQNSVTSSEDTATYTCARWDYGT 122
DB 61 KLEWMGYINSAGSTNNPSLKRISITRDTSKNQFFLQNSVTSSEDTATYTCARWDYGT 120

OY 123 YGYDFVWGQGTVT 136
DB 121 --RFAYWGQGLT 132

RESULT 8
HV60_MOUSE

HV60_MOUSE STANDARD; PRT; 116 AA.
P18531;
DT 01-NOV-1990, integrated into UniProtKB/Swiss-Prot.
DT 01-NOV-1990, sequence version 1.
DT 07-MAR-2006, entry version 39.
DE Ig heavy chain V region M315 precursor.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
OX NCBI_TaxID=10090;
RN [1].
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=BALB/cJ;
RX MEDLINE=8979149; PubMed=2499654; DOI=10.1084/jem.169.6.2007;
RA Levy N.S., Malpietro U.V., Lebecque S.G., Gearhart P.J.;
RT "Early onset of somatic mutation in immunoglobulin VH genes during the
primary immune response";
RL J. Exp. Med. 169:2007-2019(1989).
CC -----
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CC -----
CC PIR: JTO509; HVMS31.
DR PDB: 1EZV; X-ray; X=20-116.
DR Ensembl: ENSMUSG0000057048; Mus musculus.
DR InterPro: IPR007110; Ig-like.
DR InterPro: IPR003596; Ig.V.
DR InterPro: IPR013106; V-set.
DR Pfam: PF07686; V-set; 1.
DR SMART: SM00406; IG; 1.
DR PROSITE: PS00835; IG LIKE; 1.
KW 3D-structure; Immunoglobulin domain; Immunoglobulin V region; Signal.
FT SIGNAL 1 18
FT CHAIN 19 116
FT REGION 19 48
FT REGION 49 53
FT REGION 54 67
FT REGION 68 84
FT REGION 85 116
FT DISULFID 40 114
FT NON_TER 116 116
FT STRAND 21 26
FT STRAND 28 30
FT TURN 32 33
FT STRAND 34 34
FT STRAND 36 45
FT TURN 47 49
FT STRAND 50 58
FT TURN 60 61
FT STRAND 64 73
FT STRAND 76 78
FT TURN 80 85
FT STRAND 89 91
FT TURN 92 95
FT STRAND 96 101
FT STRAND 103 103
FT HELIX 106 108
SQ SEQUENCE 116 AA; 13095 MW; 4562E03E53DC9E10 CRC64;

Query Match 73.1%; Score 539; DB 1; Length 116;
Best Local Similarity 87.1%; Pred. No. 3.4e-44;
Matches 101; Conservative 7; Mismatches 8; Indels 0; Gaps 0;

OY 1 MRVILLWLFAPGILSDVQLQESGPGLVKPSQSLTCSVTGYSTSGYANNWIROP 60
DB 1 MKVLSLLYLLTALPGILSDVQLQESGPGLVKPSQSLTCSVTGYSTSGYANNWIROP 60

OY 61 GNKLEWMGYISYSGFTSYNPSLRISIFTRDTSKNQFFLQNSVTSSEDTATYTCAR 116
DB 61 GNKLEWMGYISYSGFTSYNPSLRISITRDTSKNQFFLQNSVTSSEDTATYTCAR 116

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RESULT 9
Q53VQ5_MOUSE
ID Q53VQ5_MOUSE PRELIMINARY; PRT; 119 AA.
AC Q53VQ5;
DT 24-MAY-2005, integrated into UniProtKB/TrEMBL.
DT 24-MAY-2005, sequence version 1.
DT 07-FEB-2006, entry version 4.
DE VH-D-JH region (Fragment).
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
OC Muridae; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RX MEDLINE=86136012; PubMed=3937730;
RA Ollier P., Rocca-Serra J., Somme G., These J., Fougereau M.;
RT "The idiotypic network and the internal image: possible regulation of
a germ-line network by paucigene encoded Ab2 (anti-idiotypic)
antibodies in the GAT system.";
RL EMBO J. 4:3681-3688(1985).
RN NUCLEOTIDE SEQUENCE OF 28-29.
RA Fougereau M.;
RP Submitted (NOV-1986) to the EMBL/GenBank/DBJ databases.
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CC -----
DR EMBL; X03379; CAA27101.1; -; mRNA.
DR InterPro; IPR003599; Ig.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003596; Ig_v.
DR SMART; SM00409; IG; 1.
DR SMART; SM00406; IGv; 1.
DR PROSITE; PS50835; IG LIKE; 1.
KW Immunoglobulin domain.
FT NON_TER 1
FT NON_TER 119
SQ SEQUENCE 119 AA; 13931 MW; 502E51A5213F056E CRC64;
[2]
RP NUCLEOTIDE SEQUENCE OF 28-29.
RA Fougereau M.;
RP Submitted (NOV-1986) to the EMBL/GenBank/DBJ databases.
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CC -----
DR EMBL; X03378; CAA27095.1; -; mRNA.
DR InterPro; IPR003599; Ig.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003596; Ig_v.
DR SMART; SM00409; IG; 1.
DR SMART; SM00406; IGv; 1.
DR PROSITE; PS50835; IG LIKE; 1.
KW Immunoglobulin domain.
FT NON_TER 1
FT NON_TER 119
SQ SEQUENCE 119 AA; 13931 MW; 502E51A5213F056E CRC64;
[2]
Query Match 68.4%; Score 504; DB 2; Length 119;
Best Local Similarity 81.5%; Pred. No. 8.5e-41;
Matches 97; Conservative 5; Mismatches 13; Indels 4; Gaps 2;
QY 19 DVQLQESGPGLVKPSQSLTCSVTGYSTSGYAWNWIRPFGNKLWGMGYISYSGFTSY 78
Db 1 DVQLQESGPGLVKPSQSLTCSVTGYSTSGYAWNWIRPFGNKLWGMGYISYDGSNHY 60
QY 79 NPSLRISRISFTRDTSKNQFFLQNSVTSEDATYYCAR---WDYGTYYGY-FDWWGQGT 133
Db 61 NPSLKNRISITRDTSKNQFFLQNSVTIEDATYYCARPLYRYDEEYYAMDYWGQGT 119
RESULT 10
Q53VQ1_MOUSE
ID Q53VQ1_MOUSE PRELIMINARY; PRT; 115 AA.
AC Q53VQ1;
DT 24-MAY-2005, integrated into UniProtKB/TrEMBL.
DT 24-MAY-2005, sequence version 1.
DT 07-FEB-2006, entry version 4.
DE VH-D-JH region (Fragment).
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
OC Muridae; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RX MEDLINE=86136012; PubMed=3937730;
RA Ollier P., Rocca-Serra J., Somme G., These J., Fougereau M.;
RT "The idiotypic network and the internal image: possible regulation of
a germ-line network by paucigene encoded Ab2 (anti-idiotypic)
antibodies in the GAT system.";
RL EMBO J. 4:3681-3688(1985).
RN NUCLEOTIDE SEQUENCE OF 28-29.
RA Fougereau M.;
RP Submitted (NOV-1986) to the EMBL/GenBank/DBJ databases.
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CC -----
DR EMBL; X03376; CAA27083.1; -; mRNA.
DR InterPro; IPR003599; Ig.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003596; Ig_v.
DR SMART; SM00409; IG; 1.
DR SMART; SM00406; IGv; 1.
SQ SEQUENCE 115 AA; 13257 MW; D465A5854DF459A3 CRC64;
[2]
Query Match 67.0%; Score 494; DB 2; Length 115;
Best Local Similarity 79.1%; Pred. No. 7.6e-40;
Matches 91; Conservative 8; Mismatches 16; Indels 0; Gaps 0;
QY 19 DVQLQESGPGLVKPSQSLTCSVTGYSTSGYAWNWIRPFGNKLWGMGYISYSGFTSY 78
Db 1 DVQLQESGPGLVKPSQSLTCSVTGYSTSGYAWNWIRPFGNKLWGMGFIRYDGSNNY 60
QY 79 NPSLRISRISFTRDTSKNQFFLQNSVTSEDATYYCARWDYGTYYGYFDWWGQGT 133
Db 61 NPSLKRISITRDTSKNQFFLRLNSVTIEDATYYCAVFGYDMDYYAMDYWGQGT 115
RESULT 11
Q53VR3_MOUSE
ID Q53VR3_MOUSE PRELIMINARY; PRT; 119 AA.
AC Q53VR3;
DT 24-MAY-2005, integrated into UniProtKB/TrEMBL.
DT 24-MAY-2005, sequence version 1.
DT 07-FEB-2006, entry version 4.
DE VH-D-JH region (Fragment).
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
OC Muridae; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RX MEDLINE=86136012; PubMed=3937730;
RA Ollier P., Rocca-Serra J., Somme G., These J., Fougereau M.;
RT "The idiotypic network and the internal image: possible regulation of
a germ-line network by paucigene encoded Ab2 (anti-idiotypic)
antibodies in the GAT system.";
RL EMBO J. 4:3681-3688(1985).
RN NUCLEOTIDE SEQUENCE OF 28-29.
RA Fougereau M.;
RP Submitted (NOV-1986) to the EMBL/GenBank/DBJ databases.
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CC -----
DR EMBL; X03375; CAA27082.1; -; mRNA.
DR InterPro; IPR003599; Ig.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003596; Ig_v.
DR SMART; SM00409; IG; 1.
DR SMART; SM00406; IGv; 1.
SQ SEQUENCE 115 AA; 13257 MW; D465A5854DF459A3 CRC64;
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Query Match 67.0%; Score 494; DB 2; Length 115;
Best Local Similarity 79.1%; Pred. No. 7.6e-40;
Matches 91; Conservative 8; Mismatches 16; Indels 0; Gaps 0;
QY 19 DVQLQESGPGLVKPSQSLTCSVTGYSTSGYAWNWIRPFGNKLWGMGYISYSGFTSY 78
Db 1 DVQLQESGPGLVKPSQSLTCSVTGYSTSGYAWNWIRPFGNKLWGMGFIRYDGSNNY 60
QY 79 NPSLRISRISFTRDTSKNQFFLQNSVTSEDATYYCARWDYGTYYGYFDWWGQGT 133
Db 61 NPSLKRISITRDTSKNQFFLRLNSVTIEDATYYCAVFGYDMDYYAMDYWGQGT 115
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RT "The idiotypic network and the internal image: possible regulation of
a germ-line network by paucigene encoded Ab2 (anti-idiotypic)
antibodies in the GAT system.";
RL EMBO J. 4:3681-3688(1985).
RN NUCLEOTIDE SEQUENCE OF 28-29.
RA Fougereau M.;
RP Submitted (NOV-1986) to the EMBL/GenBank/DBJ databases.
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CC -----
DR EMBL; X03379; CAA27101.1; -; mRNA.
DR InterPro; IPR003599; Ig.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003596; Ig_v.
DR SMART; SM00409; IG; 1.
DR SMART; SM00406; IGv; 1.
DR PROSITE; PS50835; IG LIKE; 1.
KW Immunoglobulin domain.
FT NON_TER 1
FT NON_TER 115
SQ SEQUENCE 115 AA; 13257 MW; D465A5854DF459A3 CRC64;
[2]
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Best Local Similarity 79.1%; Pred. No. 7.6e-40;
Matches 91; Conservative 8; Mismatches 16; Indels 0; Gaps 0;
QY 19 DVQLQESGPGLVKPSQSLTCSVTGYSTSGYAWNWIRPFGNKLWGMGYISYSGFTSY 78
Db 1 DVQLQESGPGLVKPSQSLTCSVTGYSTSGYAWNWIRPFGNKLWGMGFIRYDGSNNY 60
QY 79 NPSLRISRISFTRDTSKNQFFLQNSVTSEDATYYCARWDYGTYYGYFDWWGQGT 133
Db 61 NPSLKRISITRDTSKNQFFLRLNSVTIEDATYYCAVFGYDMDYYAMDYWGQGT 115
RESULT 11
Q53VR3_MOUSE
ID Q53VR3_MOUSE PRELIMINARY; PRT; 119 AA.
AC Q53VR3;
DT 24-MAY-2005, integrated into UniProtKB/TrEMBL.
DT 24-MAY-2005, sequence version 1.
DT 07-FEB-2006, entry version 4.
DE VH-D-JH region (Fragment).
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
OC Muridae; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RX MEDLINE=86136012; PubMed=3937730;
RA Ollier P., Rocca-Serra J., Somme G., These J., Fougereau M.;
RT "The idiotypic network and the internal image: possible regulation of
a germ-line network by paucigene encoded Ab2 (anti-idiotypic)
antibodies in the GAT system.";
RL EMBO J. 4:3681-3688(1985).
RN NUCLEOTIDE SEQUENCE OF 28-29.
RA Fougereau M.;
RP Submitted (NOV-1986) to the EMBL/GenBank/DBJ databases.
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CC -----
DR EMBL; X03376; CAA27083.1; -; mRNA.
DR InterPro; IPR003599; Ig.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003596; Ig_v.
DR SMART; SM00409; IG; 1.
DR SMART; SM00406; IGv; 1.
SQ SEQUENCE 115 AA; 13257 MW; D465A5854DF459A3 CRC64;
[2]
Query Match 67.0%; Score 494; DB 2; Length 115;
Best Local Similarity 79.1%; Pred. No. 7.6e-40;
Matches 91; Conservative 8; Mismatches 16; Indels 0; Gaps 0;
QY 19 DVQLQESGPGLVKPSQSLTCSVTGYSTSGYAWNWIRPFGNKLWGMGYISYSGFTSY 78
Db 1 DVQLQESGPGLVKPSQSLTCSVTGYSTSGYAWNWIRPFGNKLWGMGFIRYDGSNNY 60
QY 79 NPSLRISRISFTRDTSKNQFFLQNSVTSEDATYYCARWDYGTYYGYFDWWGQGT 133
Db 61 NPSLKRISITRDTSKNQFFLRLNSVTIEDATYYCAVFGYDMDYYAMDYWGQGT 115
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DP PROSITE; P50835; IG LIKE; 1.
FW Immunoglobulin domain.
FT NON_TER 1 119
FT NON_TER 119 119
SQ SEQUENCE 119 AA; 13799 MW; 36504D1665BFB59 CRC64;
Query Match 66.1%; Score 487; DB 2; Length 119;
Best Local Similarity 79.0%; Pred. No. 3.8e-39;
Matches 94; Conservative 5; Mismatches 16; Indels 4; Gaps 1;
QY 19 DVLOQSGGLVKPSQSLTSCVTGYSTSGYANWIRQFPGNKLEWGWYISYSGFTSY 78
Db 1 DVLOQSGGLVKPSQSLTSCVTGNSITSGYWNIRQFPGNKLEWGWYIKYDGNNSY 60
QY 79 NPSLSRSIFTRDTSKNQFLQNSVTSEDTATYYCARWDY-----GTTTGYGFYDVGQGT 133
Db 61 NPSLKNRISITRDTSKNQFLKNSVTTEDTATYYCARPLYFRHDEYDVMYDVGQGT 119
RESULT 12
Q53VR7_MOUSE PRELIMINARY; PRT; 120 AA.
AC Q53VR7;
DT 24-MAY-2005, integrated into UniProtKB/TrEMBL.
DT 07-FEB-2006, entry version 4.
DE VH-D-JH region (Fragment).
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
OC Muridae; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RX MEDLINE=86136012; PubMed=3937730;
RA Ollier P., Rocca-Serra J., Somme G., Theze J., Fougereau M.;
RT "The idiotypic network and the internal image: possible regulation of
RT a germ-line network by paucigenic encoded Ab2 (anti-idiotypic)
RL antibody in the GAT system.";
RL EMBO J. 4:3681-3688(1985).
RN [2]
RP NUCLEOTIDE SEQUENCE OF 28-29.
RA Fougereau M.;
RL Submitted (NOV-1986) to the EMBL/GenBank/DBJ databases.
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CC
DR EMBL; X03375; CAA27077.1; -; mRNA.
DR EMBL; X03374; CAA27071.1; -; mRNA.
DR SMR; Q53VR7; 1-120.
DR InterPro; IPR003599; Ig.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003596; Ig_v.
DR SMART; SM00409; IG; 1.
DR SMART; SM00406; IGv; 1.
DR PROSITE; P50835; IG LIKE; 1.
KW Immunoglobulin domain.
FT NON_TER 1
FT NON_TER 120
SQ SEQUENCE 120 AA; 13892 MW; 013452306EBA3BE CRC64;
Query Match 65.7%; Score 484.5; DB 2; Length 120;
Best Local Similarity 75.8%; Pred. No. 6.7e-39;
Matches 91; Conservative 8; Mismatches 16; Indels 5; Gaps 1;
QY 19 DVLOQSGGLVKPSQSLTSCVTGYSTSGYANWIRQFPGNKLEWGWYISYSGFTSY 78
Db 1 DVHLOQSGGLVKPSQSLTSCVTGYSTRGYNNWIRRFPGNKLEWGWYINDGNNY 60
QY 79 NPSLSRSIFTRDTSKNQFLQNSVTSEDTATYYCARW-----DYGTTYGFYDVGQGT 133
Db 61 NPSLKNRISITRDTSKNQFLKNSVTTEDTATYYCARLIPFSDGYDYDVMYDVGQGT 120

RESULT 13
HV62_MOUSE STANDARD; PRT; 117 AA.
ID HV62_MOUSE
AC P18533;
DT 01-NOV-1990, integrated into UniProtKB/Swiss-Prot.
DT 01-NOV-1990, sequence version 1.
DT 07-MAR-2006, entry version 37.
DE Ig heavy chain V region 733 precursor.
DE Ig heavy chain V region 733 precursor.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
OC Muridae; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=BALB/CJ;
RX MEDLINE=89279149; PubMed=2499654; DOI=10.1084/jem.169.6.2007;
RA Levy N.S., Malipiero U.V., Lebecque S.G., Gearhart P.J.;
RT "Early onset of somatic mutation in immunoglobulin VH genes during the
RT primary immune response.";
RL J. Exp. Med. 169:2007-2019(1989).
CC -!- SIMILARITY: Contains 1 Ig-like (immunoglobulin-like) domain.
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CC
DR PIR; JTO510; HWM573.
DR HSSP; P01820; IG70.
DR SMR; P18533; 19-117.
DR Ensembl; ENSMUSG00000059520; Mus musculus.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003596; Ig_v.
DR InterPro; IPR013106; V-set.
DR Pfam; PF07686; V-set; 1.
DR SMART; SM00406; IGv; 1.
DR PROSITE; P50835; IG LIKE; 1.
KW Immunoglobulin domain; Immunoglobulin V region; Signal.
FT SIGNAL 1 18
FT CHAIN 19 117
FT CHAIN 19 117
FT DOMAIN 19 >117
FT DISULFID 40 115
FT NON_TER 117 117
SQ SEQUENCE 117 AA; 13223 MW; 1595517827F976BE CRC64;
Query Match 64.7%; Score 476.5; DB 1; Length 117;
Best Local Similarity 75.2%; Pred. No. 3.9e-38;
Matches 88; Conservative 15; Mismatches 13; Indels 1; Gaps 1;
QY 1 MRVLLILLFTAPPGLSDVQLQESGPGGLVKPSQSLTSCVTGYSTSG-YANWIRQF 59
Db 1 MKMFTLLYLLTVPGILSDVQLQESGPGGLVKPSQSLTCTVTGSIITGNVRSWIRQF 60
QY 60 PGNKLEWGWYISYSGFTSYNPSLSRSIFTRDTSKNQFLQNSVTSEDTATYYCAR 116
Db 61 PGNKLEWGWYISYSAITSYNPSPKSRRTITRDTSKNQFLKNSLTAEATATYYCAR 117
RESULT 14
Q53VQ4_MOUSE PRELIMINARY; PRT; 98 AA.
ID Q53VQ4_MOUSE
AC Q53VQ4;
DT 24-MAY-2005, integrated into UniProtKB/TrEMBL.
DT 24-MAY-2005, sequence version 1.
DT 07-FEB-2006, entry version 3.
DE VH region (Fragment).
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
OC Muridae; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;

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RN NUCLEOTIDE SEQUENCE.
RP NUCLEOTIDE SEQUENCE.
RX MEDLINE=86136012; PubMed=3937730;
RA Ollier P., Rocca-Serra J., Somme G., These J., Fougereau M.;
RT "The idiotypic network and the internal image: possible regulation of
RT a germ-line network by paucigene encoded Ab2 (anti-idiotypic)
RT antibodies in the GAT system.";
RL EMBO J. 4:3681-3688(1985).
RN [2]
RP NUCLEOTIDE SEQUENCE OF 28-29.
RA Fougereau M.;
RL Submitted (NOV-1986) to the EMBL/GenBank/DBJ databases.
CC -----
CC Copyrighted by the UniProt Consortium, see http://www.uniprot.org/terms
CC Distributed under the Creative Commons Attribution-NoDerivs License
CC -----
DR EMBL; X03378; CAA27096.1; -; mRNA.
DR SMR; Q53VQ4; 1-98.
DR Ensembl; ENSMUSG0000057048; Mus musculus.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003596; Ig_V.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PS50835; IG LIKE; 1.
FT NON_TER 1
FT NON_TER 98
FT NON_TER 98
SQ SEQUENCE 98 AA; 11203 MW; 4049CF8C7E8AAE0 CRC64;

Query Match 64.2%; Score 473; DB 2; Length 98;
Best Local Similarity 89.8%; Pred. NO. 6.9e-38;
Matches 88; Conservative 4; Mismatches 6; Indels 0; Gaps 0;

QY 19 DVQLQESGGLVKPSQSLSLTCVGTGYSTSGYANNWIRQPGNKLWNGYISYSGFTSY 78
DB 1 DVQLQESGGLVKPSQSLSLTCVGTGYSTSGYANNWIRQPGNKLWNGYISYSGFTSY 78
QY 79 NPSLRSRISFTRDTSKNQFFLQLNSVTSEDATYYCAR 116
DB 61 NPSLKNRISITRDTSKNQFFLQLNSVTIEDATYYCAR 98

RESULT 15
Q53VQ9 MOUSE PRELIMINARY; PRT; 119 AA.
AC Q53VQ9
DT 24-MAY-2005, integrated into UniProtKB/TrEMBL.
DT 24-MAY-2005, sequence version 1.
DT 07-FEB-2006, entry version 4.
DE VH-D-JH region (Fragment).
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
OC Murioidea; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RX MEDLINE=86136012; PubMed=3937730;
RA Ollier P., Rocca-Serra J., Somme G., These J., Fougereau M.;
RT "The idiotypic network and the internal image: possible regulation of
RT a germ-line network by paucigene encoded Ab2 (anti-idiotypic)
RT antibodies in the GAT system.";
RL EMBO J. 4:3681-3688(1985).
RN [2]
RP NUCLEOTIDE SEQUENCE OF 28-29.
RA Fougereau M.;
RL Submitted (NOV-1986) to the EMBL/GenBank/DBJ databases.
CC -----
CC Copyrighted by the UniProt Consortium, see http://www.uniprot.org/terms
CC Distributed under the Creative Commons Attribution-NoDerivs License
CC -----
DR EMBL; X03377; CAA27089.1; -; mRNA.
DR SMR; Q53VQ9; 1-118.
DR InterPro; IPR003599; Ig.
DR InterPro; IPR007110; Ig-like.
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DR InterPro; IPR003596; Ig_v.
DR SMART; SM00409; IG; 1.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PS50835; IG LIKE; 1.
KW Immunoglobulin domain.
FT NON_TER 1
FT NON_TER 119
FT NON_TER 119
SQ SEQUENCE 119 AA; 13844 MW; 6B1BC8C7DC77E147 CRC64;

Query Match 62.8%; Score 463; DB 2; Length 119;
Best Local Similarity 74.6%; Pred. NO. 8e-37;
Matches 88; Conservative 10; Mismatches 16; Indels 4; Gaps 2;

QY 19 DVQLQESGGLVKPSQSLSLTCVGTGYSTSGYANNWIRQPGNKLWNGYISYSGFTSY 78
DB 1 DVQLQESGGLVKPSQSLSLTCVGTGYSTSGYANNWIRQPGNKLWNGYISYSGFTSY 78
QY 79 NPSLRSRISFTRDTSKNQFFLQLNSVTSEDATYYCAR---WDYGTYYCY-FDVMGQG 132
DB 61 NPSLKNRISITRDTSKNQFFLQLNSVTIEDATYYCYRPLYYRFDPEEYYATDYWGQG 118

Search completed: May 19, 2006, 17:46:30
Job time : 209.238 secs
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GenCore version 5.1.8
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OM protein - protein search, using sw model

Run on: May 19, 2006, 17:46:56 ; Search time 39.3968 Seconds
(without alignments)
302.161 Million cell updates/sec

Title: US-09-889-936A-6
Perfect score: 737
Sequence: 1 MRVLILLMLFTAPGILSDV.....WDYGTYYGYFVWGQGTTVT 136

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 650591 seqs, 87530628 residues

Total number of hits satisfying chosen parameters: 650591

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Issued Patents_AA:
1: /EMC_Celerra_SIDS3/ptodata/2/iaa/5 COMB.pap:*
2: /EMC_Celerra_SIDS3/ptodata/2/iaa/6 COMB.pap:*
3: /EMC_Celerra_SIDS3/ptodata/2/iaa/7 COMB.pap:*
4: /EMC_Celerra_SIDS3/ptodata/2/iaa/H COMB.pap:*
5: /EMC_Celerra_SIDS3/ptodata/2/iaa/PCTUS COMB.pap:*
6: /EMC_Celerra_SIDS3/ptodata/2/iaa/RE COMB.pap:*
7: /EMC_Celerra_SIDS3/ptodata/2/iaa/backfiles1.pap:

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match %	Length	DB ID	Description
1	588	79.8	137	1	US-08-137-117D-31 Sequence 31, Appl
2	588	79.8	137	1	US-08-436-717-31 Sequence 31, Appl
3	541	73.4	119	2	US-08-767-128-18 Sequence 18, Appl
4	525.5	71.3	117	1	US-08-308-494A-13 Sequence 13, Appl
5	514	69.7	118	2	US-09-065-059-11 Sequence 11, Appl
6	514	69.7	118	2	US-08-913-555-11 Sequence 11, Appl
7	510.5	69.3	114	1	US-08-111-080-23 Sequence 23, Appl
8	510.5	69.3	114	1	US-08-311-980-23 Sequence 23, Appl
9	510.5	69.3	114	5	PCT-US93-07967-23 Sequence 23, Appl
10	509.5	69.1	137	2	US-08-466-151-7 Sequence 7, Appl
11	509.5	69.1	137	2	US-08-466-163B-7 Sequence 7, Appl
12	509.5	69.1	137	2	US-09-802-096-7 Sequence 7, Appl
13	509.5	69.1	137	2	US-09-802-077-3 Sequence 7, Appl
14	509.5	69.1	137	2	US-09-925-179-3 Sequence 7, Appl
15	509	69.1	117	1	US-08-672-345C-13 Sequence 13, Appl
16	509	69.1	117	2	US-09-214-095D-13 Sequence 13, Appl
17	509	69.1	117	2	US-09-940-727B-13 Sequence 13, Appl
18	500.5	67.9	240	1	US-07-956-399-2 Sequence 2, Appl
19	500	67.8	121	1	US-08-887-352B-2 Sequence 2, Appl
20	500	67.8	121	2	US-09-109-207C-2 Sequence 2, Appl
21	500	67.8	121	2	US-09-296-005-2 Sequence 2, Appl
22	500	67.8	121	2	US-09-920-171-2 Sequence 2, Appl
23	500	67.8	121	2	US-09-716-028-2 Sequence 2, Appl
24	500	67.8	121	2	US-10-113-996-2 Sequence 2, Appl
25	500	67.8	130	2	US-08-466-151-5 Sequence 5, Appl
26	500	67.8	130	2	US-08-466-163B-5 Sequence 5, Appl

ALIGNMENTS

RESULT 1
US-08-137-117D-31
; Sequence 31, Application US/08137117D
; Patent No. 5795965
; GENERAL INFORMATION:
; APPLICANT: TSUCHIYA, Masayuki
; APPLICANT: SATO, Koh
; APPLICANT: BENDIG, Mary
; APPLICANT: JONES, Steven
; APPLICANT: SALDANHA, Jose
; TITLE OF INVENTION: RESHAPED HUMAN ANTIBODY TO HUMAN
; TITLE OF INVENTION: INTERLEUKIN-6 RECEPTOR
; NUMBER OF SEQUENCES: 156
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Foley & Lardner
; STREET: 3000 K Street, N.W., Suite 500
; CITY: Washington
; STATE: D.C.
; COUNTRY: USA
; ZIP: 20007-5109
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/137,117D
; FILING DATE: 20-DEC-1993
; CLASSIFICATION: 530
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: WO PCT/JP92/00544
; FILING DATE: 24-APR-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: JP 4-32084
; FILING DATE: 19-FEB-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: JP 3-95476
; FILING DATE: 25-APR-1991
; ATTORNEY/AGENT INFORMATION:
; NAME: WEGNER, Harold C.
; REGISTRATION NUMBER: 25,258
; REFERENCE/DOCKET NUMBER: 53466/126/AOOK
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (202)672-5300
; TELEFAX: (202)672-5399
; TELEX: 904136
; INFORMATION FOR SEQ ID NO: 31:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 137 amino acids

Sequence 5, Appli
Sequence 5, Appli
Sequence 5, Appli
Sequence 3, Appli
Sequence 3, Appli
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Sequence 13, Appli
Sequence 15, Appli
Sequence 10, Appli
Sequence 11, Appli
Sequence 100, App
Sequence 101, App
Sequence 10, App
Sequence 11, Appli
Sequence 10, Appli

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; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-137-117D-31

Query Match          79.8%; Score 588; DB 1; Length 137;
Best Local Similarity 83.8%; Pred. No. 1.le-49;
Matches 114; Conservative 8; Mismatches 12; Indels 2; Gaps 1;

QY 1 MRVLILLMFTAPPGLSDVQLQESGPGVLKPSQSLTCSVTGYSTISGVANNWIROFP 60
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Db 1 MRVLILLMFTAPPGLSDVQLQESGPGVLKPSQSLTCTVTGYSTISDHAWSIROFP 60
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QY 61 GNKLEWMCYISYSGFTSYNPSLRISFTRDTSKNQFFLQNLNSVTSEDTATYYCARWDYG 120
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Db 61 GNKLEWMCYISYSGITTYNPSLKRISITRDTSKNQFFLQNLNSVTGTDTSTYYCARSLAR 120
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QY 121 TTYGYFDVWGQGTTVT 136
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Db 121 TT--AMDYWGQGTSVT 134
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RESULT 2
US-08-436-717-31
; Sequence 31, Application US/08436717
; Patent No. 5817790
; GENERAL INFORMATION:
; APPLICANT: TSUCHIYA, Masayuki
; APPLICANT: SATO, Koh
; APPLICANT: BENDIG, Mary
; APPLICANT: JONES, Steven
; APPLICANT: SALDANHA, Jose
; TITLE OF INVENTION: RESHAPED HUMAN ANTIBODY TO HUMAN
; TITLE OF INVENTION: INTERLEUKIN-6 RECEPTOR
; NUMBER OF SEQUENCES: 158
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Foley & Lardner
; STREET: 3000 K Street, N.W., Suite 500
; CITY: Washington
; STATE: D.C.
; COUNTRY: USA
; ZIP: 20007-5109
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC Compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/436,717
; FILING DATE:
; CLASSIFICATION: 536
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/08/137,117
; FILING DATE: 20-DEC-1993
; APPLICATION NUMBER: WO PCT/Jp92/00544
; FILING DATE: 24-APR-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: JP 4-32084
; FILING DATE: 19-FEB-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: JP 3-95476
; FILING DATE: 25-APR-1991
; ATTORNEY/AGENT INFORMATION:
; NAME: WEGNER, Harold C.
; REGISTRATION NUMBER: 25,258
; REFERENCE/DOCKET NUMBER: 53466/126/AAOK
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (202) 672-5300
; TELEFAX: (202) 672-5399
; TELEX: 904136
; INFORMATION FOR SEQ ID NO: 31:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 137 amino acids

; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-436-717-31

Query Match          79.8%; Score 588; DB 1; Length 137;
Best Local Similarity 83.8%; Pred. No. 1.le-49;
Matches 114; Conservative 8; Mismatches 12; Indels 2; Gaps 1;

QY 1 MRVLILLMFTAPPGLSDVQLQESGPGVLKPSQSLTCSVTGYSTISGVANNWIROFP 60
   |||||
Db 1 MRVLILLMFTAPPGLSDVQLQESGPGVLKPSQSLTCTVTGYSTISDHAWSIROFP 60
   |||||

QY 61 GNKLEWMCYISYSGFTSYNPSLRISFTRDTSKNQFFLQNLNSVTSEDTATYYCARWDYG 120
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Db 61 GNKLEWMCYISYSGITTYNPSLKRISITRDTSKNQFFLQNLNSVTGTDTSTYYCARSLAR 120
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QY 121 TTYGYFDVWGQGTTVT 136
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Db 121 TT--AMDYWGQGTSVT 134
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RESULT 3
US-08-767-128-18
; Sequence 18, Application US/08767128
; Patent No. 6111079
; GENERAL INFORMATION:
; APPLICANT: WYLIE, DWANE E.
; APPLICANT: LOPEZ, OSVALDO
; APPLICANT: MURRAY, PETER JOSEPH
; APPLICANT: GOEBEL, PETER
; TITLE OF INVENTION: LEAD BINDING POLYPEPTIDES AND
; TITLE OF INVENTION: NUCLEOTIDES CODING THEREFORE
; NUMBER OF SEQUENCES: 46
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Merchant, Gould, Smith, Edell, Welter & Schmidt
; STREET: 3100 No. 611079west Center, 90 South Seventh St
; CITY: Minneapolis
; STATE: MN
; COUNTRY: USA
; ZIP: 55402
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSeq Version 1.5
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/767,128
; FILING DATE:
; CLASSIFICATION: 424
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER:
; FILING DATE: 04-DEC-1996
; CLASSIFICATION: 424
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: PCT/US96/09258
; FILING DATE: 05-JUN-1996
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/541,373
; FILING DATE: 10-OCT-1995
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/462,798
; FILING DATE: 05-JUN-1995
; ATTORNEY/AGENT INFORMATION:
; NAME: Carter, Charles G.
; REGISTRATION NUMBER: 35,093
; REFERENCE/DOCKET NUMBER: 8648.49USF1
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 612/371-5278
; TELEFAX: 612/332-9081
; TELEX:
; INFORMATION FOR SEQ ID NO: 18:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 137 amino acids
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LENGTH: 119 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
HYPOTHEICAL: NO
ANTI-SENSE: NO
FRAGMENT TYPE: internal
ORIGINAL SOURCE:
US-08-767-128-18

Query Match 73.4%; Score 541; DB 2; Length 119;
Best Local Similarity 87.3%; Pred. No. 3.4e-45;
Matches 103; Conservative 4; Mismatches 9; Indels 2; Gaps 1;

QY 19 DVQLQSGPLVKPSQSLTCSVTGYSTGYANWIRQFPGNKLEWGMGYISYSGFTSY 78
DB 1 DVQLQSGPLVKPSQSLTCTVTGYSTGYANWIRQFPGNKLEWGMGYISYSGTSY 60
QY 79 NPSLRISFRDTSKNQFLLQNSVTSDTATYCARWDYGTGYFDVWGGTTVT 136
DB 61 NPSLRISFRDTSKNQFLLQNSVTSDTATYCAR--CGNYPWYFDVWGGTTLT 116

RESULT 4

US-08-308-494A-13
Sequence 13, Application US/08308494A
Patent No. 5959083

GENERAL INFORMATION:
APPLICANT: Bosset, Klaus
APPLICANT: Seeman, Gerhard
TITLE OF INVENTION: Tetraivalent Bispecific Receptors, The
TITLE OF INVENTION: Preparation and Use Thereof
NUMBER OF SEQUENCES: 24
CORRESPONDENCE ADDRESS:
ADDRESSEE: Finnegan, Henderson, Farabow, Garrett &
ADDRESSEE: Dunner
STREET: 1300 I Street, N.W., Suite 700
CITY: Washington
STATE: D.C.
COUNTRY: USA
ZIP: 20005-3315

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/308,494A
FILING DATE: 21-SEP-1994
CLASSIFICATION: 424
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/891,739
FILING DATE: 01-JUN-1992
CLASSIFICATION: 424
PRIOR APPLICATION DATA:
APPLICATION NUMBER: DE P4118120.4
FILING DATE: 03-JUN-1991
ATTORNEY/AGENT INFORMATION:
NAME: Kulik, David J.
REGISTRATION NUMBER: 36,576
REFERENCE/DOCKET NUMBER: 05552-1186-02000
TELEPHONE: 202-408-4000
TELEFAX: 202-408-4400

INFORMATION FOR SEQ ID NO: 13:
SEQUENCE CHARACTERISTICS:
LENGTH: 117 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-08-308-494A-13

Query Match 71.3%; Score 525.5; DB 1; Length 117;
Best Local Similarity 85.2%; Pred. No. 1.1e-43;
Matches 98; Conservative 7; Mismatches 9; Indels 1; Gaps 1;

QY 22 LQESGGLVKPSQSLTCSVTGYSTGYANWIRQFPGNKLEWGMGYISYSGFTSYNPS 81
DB 1 LQESGDLVKPSQSLTCTVTGYSTGYSHWIRQFPGNKLEWGMGYIQSYGTTYNPS 60
QY 82 LRSRISFRDTSKNQFLLQNSVTSDTATYCARWDYGTGYFDVWGGTTVT 136
DB 61 LKSRISTRDTSKNQFLLQNSVTSDTATYCARWDY--DYHWYFDVWGGTTVT 114

RESULT 5

US-09-065-059-11
Sequence 11, Application US/09065059
Patent No. 6068841

GENERAL INFORMATION:
APPLICANT: SEINO, Ken-ichi
APPLICANT: KAVAGAKI, No. 6068841uhiko
APPLICANT: YAGITA, Hideo
APPLICANT: OKUMURA, Ko
APPLICANT: NAKATA, Motomi
TITLE OF INVENTION: THERAPEUTIC AGENT FOR HEPATITIS
NUMBER OF SEQUENCES: 18
CORRESPONDENCE ADDRESS:
ADDRESSEE: McDermott, Will & Emery
STREET: 99 Canal Center Plaza
CITY: Alexandria
STATE: Virginia
COUNTRY: USA
ZIP: 22314

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/065,059
FILING DATE:
CLASSIFICATION: 424

ATTORNEY/AGENT INFORMATION:
NAME: Bucca Ph.D., Daniel
REGISTRATION NUMBER: P-42,368
REFERENCE/DOCKET NUMBER: 50356-151
TELEPHONE: 703-518-5100
TELEFAX: 703-684-1124
INFORMATION FOR SEQ ID NO: 11:
SEQUENCE CHARACTERISTICS:
LENGTH: 118 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-09-065-059-11

Query Match 69.7%; Score 514; DB 2; Length 118;
Best Local Similarity 83.1%; Pred. No. 1.4e-42;
Matches 98; Conservative 8; Mismatches 8; Indels 4; Gaps 2;

QY 20 VOLQESGGLVKPSQSLTCSVTGYSTGYANWIRQFPGNKLEWGMGYISYSGFTSYN 79
DB 1 VOLQESGGLVKPSQSLTCSVTGYSTGYANWIRQFPGNKLEWGMGYISYSGFTSYN 60
QY 80 PSLSRISFRDTSKNQFLLQNSVTSDTATYCARWDY-GTGYFDVWGGTTVT 136
DB 61 PSLSRISFRDTSKNQFLLQNSVTSDTATYCARVYDSS---FDWGGTTVT 115

RESULT 6

US-08-913-555-11

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; Sequence 11, Application US/08913555
; Patent No. 6946255
; GENERAL INFORMATION:
; APPLICANT: KAYAGAKI, No. 6946255uhiko
; APPLICANT: YAGITA, Kideo
; APPLICANT: OKUMURA, KO
; APPLICANT: NAKATA, Motomi
; TITLE OF INVENTION: MONOCLONAL ANTIBODY SPECIFICALLY
; TITLE OF INVENTION: REACTING WITH Fas LIGAND AND PRODUCTION PROCESS THEREOF
; NUMBER OF SEQUENCES: 31
; CORRESPONDENCE ADDRESS:
; ADDRESS: McDermott, Will & Emery
; STREET: 99 Canal Center Plaza, Suite 300
; CITY: Alexandria
; STATE: Virginia
; COUNTRY: USA
; ZIP: 22314
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; FILING DATE: 19-SEP-1997
; APPLICATION NUMBER: US/08/913,555
; CLASSIFICATION: 520
; ATTORNEY/AGENT INFORMATION:
; NAME: Bucca Ph.D., Daniel
; REGISTRATION NUMBER: 42,368
; REFERENCE/DOCKET NUMBER: 50356-150
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 202-756-8600
; TELEFAX: 202-756-8699
; INFORMATION FOR SEQ ID NO: 11:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 118 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; US-08-913-555-11

Query Match 69.7%; Score 514; DB 2; Length 118;
Best Local Similarity 83.1%; Pred. No. 1.4e-42;
Matches 98; Conservative 8; Mismatches 8; Indels 4; Gaps 2;

QY 20 VOLQESGPGLVKPSQSLTCSVTGYSTGYANWIRQFPGNKLEWGWYISYSGFTSYN 79
Db 1 VOLQESGPGLVKPSQSLTCSVTGYSTGYANWIRQFPGNKLEWGWYISYDGSNNYN 60

QY 80 PSLRSRISFTRDTSKNQFFLQNLNSVTSEDATYYCARWDY-CTTYGYFDVWGQGTVT 136
Db 61 PSLKRSRISFTRDTSKNQFFLQNLNSVTSEDATYYCAVYYDGS---FDYWGQGTVT 115

RESULT 7
US-08-111-080-23
; Sequence 23, Application 08/111080
; Patent No. 555865
; GENERAL INFORMATION:
; APPLICANT: Ohno, Tsuneva
; TITLE OF INVENTION: HIV Immunotherapeutics
; NUMBER OF SEQUENCES: 38
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Marshall, O'Toole, Gerstein, Murray &
; STREET: 6300 Sears Tower, 233 S. Wacker Drive
; CITY: Chicago
; STATE: Illinois
; COUNTRY: USA
; ZIP: 60606
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/211,980
; FILING DATE:
; CLASSIFICATION: 424
; PRIOR APPLICATION DATA:
; PRIOR APPLICATION NUMBER: PCT/US92/07111
; FILING DATE: 24-AUG-1992
; APPLICATION NUMBER: 08/111,080
; FILING DATE:
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: 08/111,080
; FILING DATE:
; CLASSIFICATION: 424
; PRIOR APPLICATION DATA:
; PRIOR APPLICATION NUMBER: PCT/US92/07111
; FILING DATE: 24-AUG-1992
; MEDIUM TYPE: Floppy disk
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; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: 08/111,080
; FILING DATE:
; CLASSIFICATION: 424
; PRIOR APPLICATION DATA:
; PRIOR APPLICATION NUMBER: US 07/748,562
; FILING DATE: 22-AUG-1991
; APPLICATION NUMBER: PCT/US92/07111
; FILING DATE: 24-AUG-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/039,457
; FILING DATE: 22-APR-1993
; ATTORNEY/AGENT INFORMATION:
; NAME: Borun, Michael F.
; REGISTRATION NUMBER: 25,447
; REFERENCE/DOCKET NUMBER: 31629
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (312) 474-6300
; TELEFAX: (312) 474-0448
; TELEX: 25-3856
; INFORMATION FOR SEQ ID NO: 23:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 114 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-111-080-23

Query Match 69.3%; Score 510.5; DB 1; Length 114;
Best Local Similarity 83.1%; Pred. No. 3e-42;
Matches 98; Conservative 5; Mismatches 8; Indels 7; Gaps 1;

QY 19 DVQLQESGPGLVKPSQSLTCSVTGYSTGYANWIRQFPGNKLEWGWYISYSGFTSY 78
Db 1 EVQLQESGPGLVKPSQSLTCTVTGYSTGYANWIRQFPGNKLEWGWYISYSGSTY 60

QY 79 NPSLRSRISFTRDTSKNQFFLQNLNSVTSEDATYYCARWDYCTTYGYFDVWGQGTVT 136
Db 61 NPSLRSRISFTRDTSKNLFLLQLSSVTSEDATYYCAR-----GSFDMGQGTLT 111

RESULT 8
US-08-211-980-23
; Sequence 23, Application US/08211980
; Patent No. 5665569
; GENERAL INFORMATION:
; APPLICANT: Ohno, Tsuneva
; TITLE OF INVENTION: HIV Immunotherapeutics
; NUMBER OF SEQUENCES: 38
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Marshall, O'Toole, Gerstein, Murray &
; STREET: 6300 Sears Tower, 233 S. Wacker Drive
; CITY: Chicago
; STATE: Illinois
; COUNTRY: USA
; ZIP: 60606
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/211,980
; FILING DATE:
; CLASSIFICATION: 424
; PRIOR APPLICATION DATA:
; PRIOR APPLICATION NUMBER: PCT/US92/07111
; FILING DATE: 24-AUG-1992
; MEDIUM TYPE: Floppy disk
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; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/039,457
; FILING DATE: 22-APR-1993
; ATTORNEY/AGENT INFORMATION:
; NAME: Borun, Michael F.
; REGISTRATION NUMBER: 25,447
; REFERENCE/DOCKET NUMBER: 31629
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (312) 474-6300
; TELEFAX: (312) 474-0448
; TELEX: 25-3856
; INFORMATION FOR SEQ ID NO: 23:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 114 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-211-980-23

Query Match 69.3%; Score 510.5; DB 1; Length 114;
Best Local Similarity 83.1%; Pred.No.3e-42;
Matches 98; Conservative 5; Mismatches 8; Indels 7; Gaps 1;

QY 19 DVLOQSGGGLVXPQSLSLTCSTVTGYSITSGYAWNWIROPFGNKLSEWVGYSYSGTSY 78
Db 1 EVLQSGGGLVXPQSLSLTCVTGYSITSDYAWNWIROPFGNKLSEWVGYSYSGSTTY 60
QY 79 NPSLRISRISTRDTSKNQFFLQLNSVTSEDTATYYCARWDYGTYYGDFVWGQGTVT 136
Db 61 NPSLKRISRISTRDTSKNLFLQLSSVTSEDTATYYCAR-----GSFGDWGQGTLYT 111

RESULT 9
PCT-US93-07967-23
; Sequence 23, Application PC/TUS9307967
; GENERAL INFORMATION:
; APPLICANT: Ohno, Tsuneya
; TITLE OF INVENTION: HIV Immunotherapeutics
; NUMBER OF SEQUENCES: 38
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Marshall, O'Toole, Gerstein, Murray &
; ADDRESSEE: Borun
; STREET: 6300 Sears Tower, 233 S. Wacker Drive
; CITY: Chicago
; STATE: Illinois
; COUNTRY: USA
; ZIP: 60606
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: PCT/US93/07967
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: PCT/US92/07111
; FILING DATE: 24-AUG-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/039,457
; FILING DATE: 22-APR-1993
; ATTORNEY/AGENT INFORMATION:
; NAME: Borun, Michael F.
; REGISTRATION NUMBER: 25,447
; REFERENCE/DOCKET NUMBER: 31629
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (312) 474-6300
; TELEFAX: (312) 474-0448
; TELEX: 25-3856
; INFORMATION FOR SEQ ID NO: 23:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 114 amino acids

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Matches	98	Conservative	7	Mismatches	13	Indels	3	Gaps	1
Qy	19	DVQLQESGPGVLVKPSQSLSLCTSVTGYITSGYAMNWIROPNGKLEWNGYIYSGGSFYS	78						
Db	1	DVQHQSEPDVLVKPSQSLSLCTVTGYITSGYNRHWIROPNGKLEWNGYIHYSGSTNY	60						
Qy	79	NPSLRSRISFTRDTSKNQFFLQLNSVTSDETTATYYCAR---	135						
Db	61	NPSLKRRISITRDTSKNQFFLQLNSVTTEDTATYYCARGSIYYGSRYRYPDWCAGTTV	120						
Qy	136	T	136						
Db	121	T	121						

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RESULT 11
US-08-466-163B-7
; Sequence 7, Application US/08466163B
; Patent No. 6329509
; GENERAL INFORMATION:
; APPLICANT: Jardieu, Paula M.
; APPLICANT: Presta, Leonard G.
; TITLE OF INVENTION: Immunoglobulin Variants
; FILE REFERENCE: P0718P2C1d1
; CURRENT APPLICATION NUMBER: US/08/466,163B
; CURRENT FILING DATE: 1995-06-06
; PRIOR APPLICATION NUMBER: US 08/405,617
; PRIOR FILING DATE: 1995-03-15
; PRIOR APPLICATION NUMBER: US 08/185,899
; PRIOR FILING DATE: 1994-01-26
; PRIOR APPLICATION NUMBER: US 07/879,495
; PRIOR FILING DATE: 1992-05-07
; PRIOR APPLICATION NUMBER: US 07/744,768
; PRIOR FILING DATE: 1991-08-14
; NUMBER OF SEQ ID NOS: 64
; SEQ ID NO 7
; LENGTH: 137
; TYPE: PRT
; ORGANISM: Mus musculus
; US-08-466-163B-7

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	Query Match	69.1%	Score 509.5;	DB 2;	Length 137;
	Best Local Similarity	81.0%	Pred. No. 4.6e-42;		
	Matches 98;	Conservative 7;	Mismatches 13;	Indels 3;	Gaps 1
Qy	19	DVQLQESGPGIWKPSQSLSLTCSTGYGITSGYAWNWIROPQGNKLEWNGIYISYSGTSY	78		
Db	1	DVQKQSEPDVWKPSQSLSLTCSTGYGITSGYNRHWIRQFPGNKLWNGIYHISGTSY	60		
Qy	79	NPSLRSRISFTTRDSKNGOFFLQLNSVTSEDATYYCAR---	WDYGTYYGYFDVMWQGGTIV	135	
Db	61	NPSLKRRIISITRDSKNGOFFLQLNSVTTEDATYYCARGSIYYGSRVRYFDVMWAGTIV	120		
Qy	136	T	136		
Db	121	T	121		

RESULT 12
US-09-802-096-7
Sequence 7, Application US/09802096
Patent No. 6685939
GENERAL INFORMATION:
APPLICANT: Jardieu, Paula M.
APPLICANT: Presta, Leonard G.
TITLE OF INVENTION: Method of Preventing the Onset of Allergic Disorders (as amended)
FILE REFERENCE: P0718P2C3US
CURRENT APPLICATION NUMBER: US/09/802,096
CURRENT FILING DATE: 2001-03-08
PRIOR APPLICATION NUMBER: US 08/405,617
PRIOR FILING DATE: 1995-03-15
PRIOR APPLICATION NUMBER: US 08/185,899
PRIOR FILING DATE: 1994-01-26

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; PRIOR APPLICATION NUMBER: PCT/US92/06860
; PRIOR FILING DATE: 1992-08-14
; PRIOR APPLICATION NUMBER: US 07/879,495
; PRIOR FILING DATE: 1992-05-07
; PRIOR APPLICATION NUMBER: US 07/744,768
; PRIOR FILING DATE: 1991-08-14
; NUMBER OF SEQ ID NOS: 64
; SEQ ID NO 7
; LENGTH: 137
; TYPE: prt
; ORGANISM: Mus musculus
; US-09-802-096-7

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Query Match	69.1%;	Score 509.5;	DB 2;	Length 137;
Best Local Similarity	81.0%;	Pred. No. 4.6e-42;		
Matches 98;	Conservative 7;	Mismatches 13;	Indels 3;	Gaps 1
Qy	19	DVQLQESGPGLVKPSQSLSTCTSGYVTSITSGYAWNMIROPPGNKLEWNGYISYSGGTSY	78	
Db	1	DVQHQESEPLVKPSQSLSTCTVTGISTGYNRHWIRQPPGNKLEWNGYIHYSGSTNY	60	
Qy	79	NPSLRSRISFTRDTSKNQOFFLQLNSVTSIEDATYYCAR---	WDYGTTTYGYFDVWQGGTTV	135
Db	61	NPSLKRRIISITRDTSKNQOFFLQLNSVITEDATYYCARGSIYYGSRVRYFDVWQAGTTV	120	
Qy	136	T	136	
Db	121	T	121	

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RESULT 13
US-09-802-077-7
; Sequence 7, Application US/09802077
; Patent No. 6699472
; GENERAL INFORMATION:
; APPLICANT: Jardieu, Paula M.
; APPLICANT: Presta, Leonard G.
; TITLE OF INVENTION: Method of Treating Allergic Disorders (as amended)
; FILE REFERENCE: P071812C2US
; CURRENT APPLICATION NUMBER: US/09/802,077
; CURRENT FILING DATE: 2001-03-08
; PRIOR APPLICATION NUMBER: US 08/405,617
; PRIOR FILING DATE: 1995-03-15
; PRIOR APPLICATION NUMBER: US 08/185,899
; PRIOR FILING DATE: 1994-01-26
; PRIOR APPLICATION NUMBER: PCT/US92/06860
; PRIOR FILING DATE: 1992-08-14
; PRIOR APPLICATION NUMBER: US 07/879,495
; PRIOR FILING DATE: 1992-05-07
; PRIOR APPLICATION NUMBER: US 07/744,768
; PRIOR FILING DATE: 1991-08-14
; NUMBER OF SEQ ID NOS: 64
; SEQ ID NO 7
; LENGTH: 137
; TYPE: PRT
; ORGANISM: Mus musculus
US-09-802-077-7

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	Query Match	69.1%; Score 509.5; DB 2;	Length 137;
	Best Local Similarity 81.0%;	Pred. No. 4.6e-42;	
Matches	96; Conservative 7;	Mismatches 13;	Indels 3; Gaps 1
Qy	19 DVLOESGPGGLVKPSQSLSLTCSVTGSITSGYAWNMIRPPGNKLEWGMVSIYSGGTSY	78	
Dd	1 DVHQESEPDLVKPSSQLSTCTVGISITSGYNRWIRPPGNKLEWGMVIHHSGSTNY	60	
Qy	79 NPSLRSRISFTRDTSKNQFFLQLNSVISEDATYYCAR---	WDYGTTTYGYFDVMQGQTTV	135
Dd	61 NPSLKGRISITRDTSKNQFFLQLNSVITEDATYYCARGSIYYGSRVRYFYEDVMCAGTTV	120	
Qy	136 T 136		
Dd	121 T 121		

RESULT 14
US-09-925-179-7
Sequence 7, Application US/09925179
Patent No. 6914129
GENERAL INFORMATION:
APPLICANT: Jardiou, Paula M.
TITLE OF INVENTION: Anti-IGE Antibodies (as amended)
FILE REFERENCE: P0718P2C1D1C1US
CURRENT APPLICATION NUMBER: US/09/925,179
CURRENT FILING DATE: 2001-08-08
PRIOR APPLICATION NUMBER: US 08/466,163
PRIOR FILING DATE: 1995-06-06
PRIOR APPLICATION NUMBER: US 08/405,617
PRIOR FILING DATE: 1995-03-15
PRIOR APPLICATION NUMBER: US 08/185,899
PRIOR FILING DATE: 1994-01-26
PRIOR APPLICATION NUMBER: PCT/US92/06860
PRIOR FILING DATE: 1992-08-14
PRIOR APPLICATION NUMBER: US 07/879,495
PRIOR FILING DATE: 1992-05-07
PRIOR APPLICATION NUMBER: US 07/744,768
PRIOR FILING DATE: 1991-08-14
NUMBER OF SEQ ID NOS: 68
SEQ ID NO 7
LENGTH: 137
TYPE: PRT
ORGANISM: Mus musculus
US-09-925-179-7

Query Match 69.1%; Score 509.5; DB 2; Length 137;
Best Local Similarity 81.0%; Pred. No. 4.6e-42;
Matches 98; Conservative 7; Mismatches 13; Indels 3; Gaps 1;
QY 19 DVQLQESGPGVLVKPSQSLTCSVTGYSITSGYANNWIRQFPGNKLEWNGYISYSGFTSY 78
Db 1 DVQHQSEPDVLVKPSQSLTCTVTGYSITSGYNNRHWRQFPGNKLEWNGYIHYSGTNY 60
QY 79 NPSLSRISFTTRDTSKNQFFLQNSVTSEDATYYCAR---WDYGTTCYFDFVWGQGTIV 135
Db 61 NPSLKRISITRDTSKNQFFLQNSVTSEDATYYCARSGSIYYGSRVYFDFVWGAGTTV 120
QY 136 T 136
Db 121 T 121

RESULT 15
US-08-672-345C-13
Sequence 13, Application US/08672345C
Patent No. 5948658
GENERAL INFORMATION:
APPLICANT: Landry Donald, W.
TITLE OF INVENTION: ANTI-COCAINE CATALYTIC ANTIBODY
NUMBER OF SEQUENCES: 108
CORRESPONDENCE ADDRESS:
ADDRESSEE: Cooper and Dunham LLP
STREET: 1185 Avenue of the Americas
CITY: New York
STATE: New York
COUNTRY: USA
ZIP: 10036
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/672,345C
FILING DATE: 24-JUN-1996
CLASSIFICATION: 435

ATTORNEY/AGENT INFORMATION:
NAME: White, John P.
REGISTRATION NUMBER: 28,678
REFERENCE/DOCKET NUMBER: 0575/51400
TELECOMMUNICATION INFORMATION:
TELEPHONE: 212-278-0400
TELEFAX: 212-391-0525
INFORMATION FOR SEQ ID NO: 13:
SEQUENCE CHARACTERISTICS:
LENGTH: 117 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-672-345C-13
Query Match 69.1%; Score 509; DB 1; Length 117;
Best Local Similarity 82.2%; Pred. No. 4.3e-42;
Matches 97; Conservative 7; Mismatches 10; Indels 4; Gaps 2;
QY 19 DVQLQESGPGVLVKPSQSLTCSVTGYSITSGYANNWIRQFPGNKLEWNGYISYSGFTSY 78
Db 1 DVQLQESGPGVLVKPSQSLTCTVTGYSITSDYANNWIRQFPGNKLEWNGYIRYSGITRY 60
QY 79 NPSLSRISFTTRDTSKNQFFLQNSVTSEDATYYCARWDYGTTCYFDFVWGQGTIV 136
Db 61 NPSLKRISITRDTSKNKFFLQNSVTSEDATYYCVRIHY---YGYGN-WQGGTTLT 114
Search completed: May 19, 2006, 17:48:42
Job time : 40.3968 secs

GenCore version 5.1.8
Copyright (c) 1993 - 2006 Bioceleration Ltd.

OM protein - protein search, using sw model

Run on: May 19, 2006, 17:47:39 ; Search time 133.841 Seconds
(without alignments)
470.686 Million cell updates/sec

Title: US-09-889-936A-6
Perfect score: 737
Sequence: 1 MRVLILLMLFTAPPGILSDV.....WDYGTGYFDVWGQGTTVT 136

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 2097797 seqs, 463214858 residues

Total number of hits satisfying chosen parameters: 2097797

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Published Applications_AA_Main:*
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2: /EMC_Celerra_SIDS3/ptodata/2/pubpaa/US08_PUBCOMB.pep.*
3: /EMC_Celerra_SIDS3/ptodata/2/pubpaa/US09_PUBCOMB.pep.*
4: /EMC_Celerra_SIDS3/ptodata/2/pubpaa/US10A_PUBCOMB.pep.*
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6: /EMC_Celerra_SIDS3/ptodata/2/pubpaa/US11_PUBCOMB.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	630	85.5	141	3	US-09-791-551-109
2	627.5	85.1	468	5	US-10-943-640-4
3	588	79.8	137	5	US-10-837-904-31
4	564.5	76.6	144	3	US-09-791-551-119
5	554	75.2	127	5	US-10-735-916A-52
6	554	75.2	127	6	US-11-012-353-52
7	544	73.8	121	4	US-10-310-674A-36
8	544	73.8	121	4	US-10-389-679-12
9	544	73.8	121	5	US-10-946-836A-12
10	539.5	73.2	730	6	US-11-035-599-30
11	539.5	73.2	730	6	US-11-035-599-29
12	539.5	73.2	761	6	US-11-035-599-29
13	539.5	73.2	762	6	US-11-035-599-28
14	535.5	72.7	140	3	US-09-874-141-53
15	535.5	72.3	115	4	US-10-308-817-131
16	532.5	72.3	115	4	US-10-453-698-131
17	532.5	72.3	115	4	US-10-453-698-131
18	527.5	71.6	118	5	US-10-735-916A-70
19	527.5	71.6	118	6	US-11-012-353-70
20	526	71.4	117	5	US-10-816-938-29
21	522	70.8	113	4	US-10-741-657A-19
22	518.5	70.4	118	4	US-10-184-300A-3
23	516	70.0	117	5	US-10-735-916A-69
24	516	70.0	117	6	US-11-012-353-69
25	512.5	69.5	136	3	US-09-858-349-2
26	512	69.5	113	4	US-10-741-657A-21
27	510	69.2	265	4	US-10-689-006-22

28	509.5	69.1	137	3	US-09-802-077-7	Sequence 7, Appli
29	509.5	69.1	137	3	US-09-802-096-7	Sequence 7, Appli
30	509.5	69.1	137	3	US-09-925-179-7	Sequence 7, Appli
31	509.5	69.1	137	5	US-10-968-237-7	Sequence 7, Appli
32	509	69.1	117	3	US-09-940-727B-13	Sequence 13, Appli
33	509	69.1	119	4	US-10-713-248-3	Sequence 3, Appli
34	509	69.1	119	4	US-10-713-248-7	Sequence 7, Appli
35	508.5	69.0	118	5	US-10-735-916A-71	Sequence 71, Appli
36	508.5	69.0	118	6	US-11-012-353-71	Sequence 71, Appli
37	502.5	68.2	118	4	US-10-372-481-17	Sequence 17, Appli
38	502.5	68.2	118	4	US-10-371-797-17	Sequence 17, Appli
39	501	68.0	135	5	US-10-735-916A-77	Sequence 77, Appli
40	501	68.0	135	6	US-11-012-353-77	Sequence 77, Appli
41	500	67.8	121	3	US-09-920-171-2	Sequence 2, Appli
42	500	67.8	121	4	US-10-113-996-2	Sequence 2, Appli
43	500	67.8	121	5	US-10-791-619-2	Sequence 2, Appli
44	500	67.8	130	3	US-09-802-077-5	Sequence 5, Appli
45	500	67.8	130	3	US-09-802-096-5	Sequence 5, Appli

ALIGNMENTS

RESULT 1

US-09-791-551-109
; Sequence 109, Application US/09791551
; Publication No. US20030235584A1
; GENERAL INFORMATION:
; APPLICANT: KLOETZER, WILLIAM S.
; APPLICANT: HANNA, NABIL
; TITLE OF INVENTION: METHOD FOR PREPARING ANTI-MIF ANTIBODIES
; FILE REFERENCE: 037003/0277869
; CURRENT APPLICATION NUMBER: US/09/791,551
; CURRENT FILING DATE: 2001-02-26
; PRIOR APPLICATION NUMBER: 60/185,390
; PRIOR FILING DATE: 2000-02-28
; PRIOR APPLICATION NUMBER: 60/233,625
; PRIOR FILING DATE: 2000-09-18
; NUMBER OF SEQ ID NOS: 119
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 109
; LENGTH: 141
; TYPE: PRT
; ORGANISM: Mus sp.
US-09-791-551-109

Query Match	85.5%;	Score 630;	DB 3;	Length 141;
Best Local Similarity	86.8%;	Pred. No. 28-49;	12;	Indels 0;
Matches	118;	Conservative	6;	Mismatches 0;
Gaps	0;			
Qy	1	MRVLILLMLFTAPPGILSDVQLQESGPGVLKPKSQSLSLTCSVTGYSITSGYAMNWIQFP	60	
Db	1	MRVLILLMLFTAPPGILSDVQLQESGPGVLKPKSQSLSLTCTVTGSSITSDYAHWIRQFP	60	
Qy	61	GNKLEWMGYISVSGTSTNPSLRISRTDTSKNQKQFQLQNSVTSDATYTCARWDVG	120	
Db	61	GNKLEWMGYISVSGTSTNPSLRISRTDTSKNQKQFQLQNSVTSDATYTCAREAYG	120	
Qy	121	TTYGYFDVWGQGTTVT	136	
Db	121	YDVGYFDVWGQGTTLT	136	

RESULT 2

US-10-943-640-4
; Sequence 4, Application US/10943640
; Publication No. US20050152907A1
; GENERAL INFORMATION:
; APPLICANT: LIANG, Tony W.
; APPLICANT: LOO, Deryk T.
; APPLICANT: XU, Xisolin
; TITLE OF INVENTION: KID3 AND KID3 ANTIBODIES THAT BIND
; THERETO

```
; FILE REFERENCE: 415072002700
; CURRENT APPLICATION NUMBER: US/10/943,640
; CURRENT FILING DATE: 2004-09-17
; PRIOR APPLICATION NUMBER: US 60/504,441
; PRIOR FILING DATE: 2003-09-18
; NUMBER OF SEQ ID NOS: 4
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 4
; LENGTH: 468
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetic Construct
US-10-943-640-4

Query Match      85.1%; Score 627.5; DB 5; Length 468;
Best Local Similarity 87.5%; Pred. No. 1.2e-48;
Matches 119; Conservative 6; Mismatches 10; Indels 1; Gaps 1;

QY 1 MRVLILLWLTAFPGILSDVQLQESGPGLVKPSQSLSLTCSVTGYSTSGYAWNNIROFP 60
Db 1 MGVLILLWLTAFPGILSDVQLQESGPGLVKPSQSLSLTCTVTGYSTSDYAWNNIROFP 60
QY 61 GNKLEWGYISYSGFTSYNPSLRISFTRDTSKNQFFLQLNSVTSEDTATYYCARWDYG 120
Db 61 GNKLEWGYISYSGFTSYNPSLRISFTRDTSKNQFFLQLNSVTSEDTATYYCARFYR 120
QY 121 TTYGYFDVWGQTTVT 136
Db 121 YA-DYFDYWGQTTLT 135

RESULT 3
US-10-837-904-31
; Sequence 31, Application US/10837904
; Publication No. US20050142635A1
; GENERAL INFORMATION:
; APPLICANT: TSUCHIYA, Masayuki
; BENDIG, Mary Margaret
; JONES, Steven Tarran
; SALDANHA, Jose William
; TITLE OF INVENTION: RESHAPED HUMAN ANTIBODY TO HUMAN
; INTERLEUKIN-6 RECEPTOR
; NUMBER OF SEQUENCES: 134
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: FOLEY & LARDNER
; STREET: 3000 K Street, N.W.
; CITY: Washington
; STATE: D.C.
; COUNTRY: U.S.A.
; ZIP: 20007-5109
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/10/837,904
; FILING DATE: 04-May-2004
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/09/114,285
; FILING DATE: 13-Jul-1998
; APPLICATION NUMBER: US 08/436,717
; FILING DATE: 08-MAY-1995
; APPLICATION NUMBER: US 08/137,117
; FILING DATE: 20-DEC-1993
; APPLICATION NUMBER: WO PCT/JP92/00544
; FILING DATE: 24-APR-1992
; APPLICATION NUMBER: JP 4-32084
; FILING DATE: 19-FEB-1992
; APPLICATION NUMBER: JP 3-95476
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; FILING DATE: 25-APR-1991
; ATTORNEY/AGENT INFORMATION:
; NAME: Wegner, Harold C.
; REGISTRATION NUMBER: 25,258
; REFERENCE/DOCKET NUMBER: 53466/234
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (202) 672-5300
; TELEFAX: (202) 672-5399
; INFORMATION FOR SEQ ID NO: 31:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 137 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; SEQUENCE DESCRIPTION: SEQ ID NO: 31:
US-10-837-904-31

Query Match      79.8%; Score 588; DB 5; Length 137;
Best Local Similarity 83.8%; Pred. No. 1.2e-45;
Matches 114; Conservative 8; Mismatches 12; Indels 2; Gaps 1;

QY 1 MRVLILLWLTAFPGILSDVQLQESGPGLVKPSQSLSLTCSVTGYSTSGYAWNNIROFP 60
Db 1 MRVLILLWLTAFPGILSDVQLQESGPGLVKPSQSLSLTCTVTGYSTSDHAWNNIROFP 60
QY 61 GNKLEWGYISYSGFTSYNPSLRISFTRDTSKNQFFLQLNSVTSEDTATYYCARWDYG 120
Db 61 GNKLEWGYISYSGFTSYNPSLRISITRDTSKNQFFLQLNSVTGTSTYYCARSLAR 120
QY 121 TTYGYFDVWGQTTVT 136
Db 121 TT--AMDYWGQTSVT 134

RESULT 4
US-09-791-551-119
; Sequence 119, Application US/09791551
; Publication No. US20030235584A1
; GENERAL INFORMATION:
; APPLICANT: KLOETZER, WILLIAM S.
; APPLICANT: HANNA, NABIL
; TITLE OF INVENTION: METHOD FOR PREPARING ANTI-MIF ANTIBODIES
; FILE REFERENCE: 037003/0277869
; CURRENT APPLICATION NUMBER: US/09/791,551
; CURRENT FILING DATE: 2001-02-26
; PRIOR APPLICATION NUMBER: 60/185,390
; PRIOR FILING DATE: 2000-02-28
; PRIOR APPLICATION NUMBER: 60/233,625
; PRIOR FILING DATE: 2000-09-18
; NUMBER OF SEQ ID NOS: 119
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 119
; LENGTH: 144
; TYPE: PRT
; ORGANISM: Mus sp.
US-09-791-551-119

Query Match      76.6%; Score 564.5; DB 3; Length 144;
Best Local Similarity 78.4%; Pred. No. 1.8e-43;
Matches 109; Conservative 9; Mismatches 18; Indels 3; Gaps 1;

QY 1 MRVLILLWLTAFPGILSDVQLQESGPGLVKPSQSLSLTCSVTGYSTSGYAWNNIROFP 60
Db 1 MVLISLLYLLTAIFGILSDVQLQESGPGLVKPSQSLSLTCSVTGYSTSGYAWNNIROFP 60
QY 61 GNKLEWGYISYSGFTSYNPSLRISFTRDTSKNQFFLQLNSVTSEDTATYYCARWD-- 118
Db 61 GNKLEWGYISYSGSKSHNPSLRNRSITRDPKSKNQFFLKLNSVTTEDTATYYCARGKI 120
QY 119 -YGTITYGYFDVWGQTTVT 136
Db 121 FYGSSYDFPAYWGQTLVT 139
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1
RESULT 5
US-10-735-916A-52
; Sequence 52, Application US/10735916A
; Publication No. US20050084906A1
; GENERAL INFORMATION:
; APPLICANT: GOETSCH, Liliane
; APPLICANT: CORVAIA, Nathalie
; APPLICANT: LEGER, Olivier
; APPLICANT: DUFLOS, Alain
; APPLICANT: BECK, Alain
; APPLICANT: HAEUW, Jean-Francois
; TITLE OF INVENTION: NOVEL ANTI-IGF-IR ANTIBODIES AND USES THEREOF
; FILE REFERENCE: 017753-183
; CURRENT APPLICATION NUMBER: US/10/735, 916A
; CURRENT FILING DATE: 2003-12-16
; PRIOR APPLICATION NUMBER: FR 03/08 538
; PRIOR FILING DATE: 2003-07-11
; PRIOR APPLICATION NUMBER: PCT/FR 03/00 178
; PRIOR FILING DATE: 2003-01-20
; PRIOR APPLICATION NUMBER: FR 02/00 653
; PRIOR FILING DATE: 2002-01-18
; PRIOR APPLICATION NUMBER: FR 02/00 654
; PRIOR FILING DATE: 2002-01-18
; PRIOR APPLICATION NUMBER: FR 02/05 753
; PRIOR FILING DATE: 2002-05-07
; NUMBER OF SEQ ID NOS: 156
; SOFTWARE: Patentin Ver. 2.1
; SEQ ID NO 52
; LENGTH: 127
; TYPE: PRT
; ORGANISM: Mus musculus
US-10-735-916A-52

Query Match 75.2%; Score 554; DB 5; Length 127;
Best Local Similarity 82.0%; Pred. No. 1.4e-42;
Matches 105; Conservative 6; Mismatches 13; Indels 4; Gaps 2;

QY 9 LFTAPGILSDVQLQESGPGLVKPSQSLTCSVTGYSTSGYANNWIRQFPGNKLEWMG 68
DB 1 LLTAIPGILSDVQLQESGPGLVKPSQSLTCSVTGYSTGGYLLWNWIRQFPGNKLEWMG 60

QY 69 YISYSGFTSYNPSLRISRTSDTSKNQFFLOLNSVTSEDTATYYCARWDYGTYYGYFDV 128
DB 61 YISYDGTNNYKPSLKDRIISITRDTSKNQFFKLNSVTNEDTATYYCAR--YGRV--FFDY 116

QY 129 WQGQTTVT 136
DB 117 WQGQTTLT 124

RESULT 6
US-11-012-353-52
; Sequence 52, Application US/11012353
; Publication No. US20050249730A1
; GENERAL INFORMATION:
; APPLICANT: GOETSCH, LILIANE
; APPLICANT: CORVAIA, NATHALIE
; APPLICANT: DUFLOS, ALAIN
; APPLICANT: HAEUW, JEAN-FRANCOIS
; APPLICANT: LEGER, OLIVIER
; APPLICANT: BECK, ALAIN
; TITLE OF INVENTION: NOVEL ANTI-IGF-IR AND/OR ANTI-INSULIN/IGF-I HYBRID
; FILE REFERENCE: 017753-198
; CURRENT APPLICATION NUMBER: US/11/012, 353
; CURRENT FILING DATE: 2004-12-16
; PRIOR APPLICATION NUMBER: 10/735, 916
; PRIOR FILING DATE: 2003-12-16
; PRIOR APPLICATION NUMBER: FR 0308538
; PRIOR FILING DATE: 2003-07-11
; PRIOR APPLICATION NUMBER: PCT/FR03/00178
; PRIOR FILING DATE: 2003-01-20

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; PRIOR APPLICATION NUMBER: FR 0205753
; PRIOR FILING DATE: 2002-05-07
; PRIOR APPLICATION NUMBER: FR 0200653
; PRIOR FILING DATE: 2002-01-18
; PRIOR APPLICATION NUMBER: FR 0200654
; PRIOR FILING DATE: 2002-01-18
; NUMBER OF SEQ ID NOS: 162
; SOFTWARE: Patentin Ver. 3.3
; SEQ ID NO 52
; LENGTH: 127
; TYPE: PRT
; ORGANISM: Mus musculus
US-11-012-353-52

Query Match 75.2%; Score 554; DB 6; Length 127;
Best Local Similarity 82.0%; Pred. No. 1.4e-42;
Matches 105; Conservative 6; Mismatches 13; Indels 4; Gaps 2;

QY 9 LFTAPGILSDVQLQESGPGLVKPSQSLTCSVTGYSTSGYANNWIRQFPGNKLEWMG 68
DB 1 LLTAIPGILSDVQLQESGPGLVKPSQSLTCSVTGYSTGGYLLWNWIRQFPGNKLEWMG 60

QY 69 YISYSGFTSYNPSLRISRTSDTSKNQFFLOLNSVTSEDTATYYCARWDYGTYYGYFDV 128
DB 61 YISYDGTNNYKPSLKDRIISITRDTSKNQFFKLNSVTNEDTATYYCAR--YGRV--FFDY 116

QY 129 WQGQTTVT 136
DB 117 WQGQTTLT 124

RESULT 7
US-10-310-674A-36
; Sequence 36, Application US/10310674A
; Publication No. US20030166860A1
; GENERAL INFORMATION:
; APPLICANT: TeGenero GmbH
; TITLE OF INVENTION: Peptide Or Protein Containing A C'-D Loop Of The CD28 Receptor
; FILE REFERENCE: 00140/004001
; CURRENT APPLICATION NUMBER: US/10/310, 674A
; CURRENT FILING DATE: 2002-12-04
; NUMBER OF SEQ ID NOS: 44
; SOFTWARE: Patentin version 3.2
; SEQ ID NO 36
; LENGTH: 121
; TYPE: PRT
; ORGANISM: Artificial
; FEATURE:
; OTHER INFORMATION: No. US20030166860A1e1 Sequence
US-10-310-674A-36

Query Match 73.8%; Score 544; DB 4; Length 121;
Best Local Similarity 87.3%; Pred. No. 1.1e-41;
Matches 103; Conservative 4; Mismatches 11; Indels 0; Gaps 0;

QY 19 DVQLQESGPGLVKPSQSLTCSVTGYSTSGYANNWIRQFPGNKLEWMGYISYSGFTSY 78
DB 1 DVQLQESGPGLVKPSQSLTCTVTGYSTSDYANNWIRQFPGNKLEWMGYIRYSGSTSY 60

QY 79 NPSLSRISRTSDTSKNQFFLOLNSVTSEDTATYYCARWDYGTYYGYFDVWQGQTTVT 136
DB 61 NPSLSRISRTSDTSKNQFFLOLNSVTEDTATYYCARDWPRPSYWFYFDVWAGTTVT 118

RESULT 8
US-10-389-679-12
; Sequence 12, Application US/10389679
; Publication No. US20040092718A1
; GENERAL INFORMATION:
; APPLICANT: TeGenero GmbH
; APPLICANT: TeGenero AG
; APPLICANT: HUNIG, Thomas

```

; TITLE OF INVENTION: Use of a CD28 Binding Substance for Making a Pharmaceutical
; FILE REFERENCE: 00140/009001, TEG/US/0302
; CURRENT APPLICATION NUMBER: US/10/389,679
; CURRENT FILING DATE: 2003-03-13
; PRIOR APPLICATION NUMBER: DE 102 12 108.7
; PRIOR FILING DATE: 2002-03-13
; NUMBER OF SEQ ID NOS: 19
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 12
; LENGTH: 121
; TYPE: PRT
; ORGANISM: artificial
; NAME/KEY: misc_feature
; LOCATION: (1)..(121)
; OTHER INFORMATION: mab
US-10-389-679-12

Query Match 73.8%; Score 544; DB 4; Length 121;
Best Local Similarity 87.3%; Pred. No. 1.1e-41;
Matches 103; Conservative 4; Mismatches 11; Indels 0; Gaps 0;
QY 19 DVQLQESGPGLVKPSQSLTCSVTGYISITSGYANNWIRQFPGNKLEWMGYISYSGFTSY 78
DB 1 DVQLQESGPGLVKPSQSLTCTVTGYISITSDYANNWIRQFPGNKLEWMGYIRYSGSTSY 60
QY 79 NPSLSRISFTTRDTSKNQFFLQNSVTSEDATYYCARWDYGTYYGYFDVWGQGTVT 136
DB 61 NPSLSRISITRDTSKNQFFLQNSVTTEDATYYCARDWPRPSYWFYFDVWGAGTTVT 118

RESULT 9

US-10-988-207-12
; Sequence 12, Application US/10988207
; Publication No. US20060008457A1
; GENERAL INFORMATION:
; APPLICANT: TeGenero AG
; APPLICANT: Hanke, Thomas
; TITLE OF INVENTION: USE OF AN EFFECTIVE SUBSTANCE BINDING TO CD28 FOR PRODUCING A
; FILE REFERENCE: TEG/US/0409
; CURRENT APPLICATION NUMBER: US/10/988,207
; CURRENT FILING DATE: 2004-11-12
; PRIOR APPLICATION NUMBER: DE 103 52 900.4
; PRIOR FILING DATE: 2003-11-11
; NUMBER OF SEQ ID NOS: 28
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 12
; LENGTH: 121
; TYPE: PRT
; ORGANISM: Artificial
; FEATURE:
; OTHER INFORMATION: mab 5.11a partial sequence
US-10-988-207-12

Query Match 73.8%; Score 544; DB 5; Length 121;
Best Local Similarity 87.3%; Pred. No. 1.1e-41;
Matches 103; Conservative 4; Mismatches 11; Indels 0; Gaps 0;
QY 19 DVQLQESGPGLVKPSQSLTCSVTGYISITSGYANNWIRQFPGNKLEWMGYISYSGFTSY 78
DB 1 DVQLQESGPGLVKPSQSLTCTVTGYISITSDYANNWIRQFPGNKLEWMGYIRYSGSTSY 60
QY 79 NPSLSRISFTTRDTSKNQFFLQNSVTSEDATYYCARWDYGTYYGYFDVWGQGTVT 136
DB 61 NPSLSRISITRDTSKNQFFLQNSVTTEDATYYCARDWPRPSYWFYFDVWGAGTTVT 118

RESULT 10

US-10-946-836A-12
; Sequence 12, Application US/10946836A
; Publication No. US20060009382A1

; GENERAL INFORMATION:
; APPLICANT: TeGenero AG
; APPLICANT: Hanke, Thomas
; APPLICANT: Lin, Chia-Huey
; TITLE OF INVENTION: USE OF A CD28 BINDING PHARMACEUTICAL SUBSTANCE FOR MAKING A
; FILE REFERENCE: 7003/25, TEG/US/0407
; CURRENT APPLICATION NUMBER: US/10/946,836A
; CURRENT FILING DATE: 2004-09-22
; PRIOR APPLICATION NUMBER: DE 103 45 008.4
; PRIOR FILING DATE: 2003-09-22
; PRIOR APPLICATION NUMBER: DE 103 49 371.9
; NUMBER OF SEQ ID NOS: 19
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 12
; LENGTH: 121
; TYPE: PRT
; ORGANISM: Artificial
; FEATURE:
; OTHER INFORMATION: monoclonal antibody 9D7 partial sequence
US-10-946-836A-12

Query Match 73.8%; Score 544; DB 5; Length 121;
Best Local Similarity 87.3%; Pred. No. 1.1e-41;
Matches 103; Conservative 4; Mismatches 11; Indels 0; Gaps 0;
QY 19 DVQLQESGPGLVKPSQSLTCSVTGYISITSGYANNWIRQFPGNKLEWMGYISYSGFTSY 78
DB 1 DVQLQESGPGLVKPSQSLTCTVTGYISITSDYANNWIRQFPGNKLEWMGYIRYSGSTSY 60
QY 79 NPSLSRISFTTRDTSKNQFFLQNSVTSEDATYYCARWDYGTYYGYFDVWGQGTVT 136
DB 61 NPSLSRISITRDTSKNQFFLQNSVTTEDATYYCARDWPRPSYWFYFDVWGAGTTVT 118

RESULT 11

US-11-035-599-30
; Sequence 30, Application US/11035599
; Publication No. US20050158829A1
; GENERAL INFORMATION:
; APPLICANT: Fandl, James
; APPLICANT: Chen, Gang
; APPLICANT: Papadopoulos, Nicholas
; APPLICANT: Aldrich, Thomas F.
; TITLE OF INVENTION: Fusion Polypeptides Capable of
; FILE REFERENCE: 1080A
; CURRENT APPLICATION NUMBER: US/11/035,599
; CURRENT FILING DATE: 2005-01-14
; PRIOR APPLICATION NUMBER: 60/536,968
; PRIOR FILING DATE: 2004-01-16
; NUMBER OF SEQ ID NOS: 53
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 30
; LENGTH: 730
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetic
US-11-035-599-30

Query Match 73.2%; Score 539.5; DB 6; Length 730;
Best Local Similarity 84.0%; Pred. No. 1.8e-40;
Matches 100; Conservative 11; Mismatches 5; Indels 3; Gaps 2;
QY 20 VQLQESGPGLVKPSQSLTCSVTGYISITSGYANNWIRQFPGNKLEWMGYISYSGFTSY 79
DB 34 VKLEESGPGLVKPSQSLTCTVTGYISITSDYANNWIRQFPGNKLEWMGYINYSITSYN 93
QY 80 PSLRSRISFTTRDTSKNQFFLQNSVTSEDATYYCARWDYGTYYGYF--DVGQGTVT 136
DB 94 PSLRSRISITRDTSKNQFFLQNSVTTEDATYYCARY-YGSSYNYGMDYWGQGTSVT 151

RESULT 12

US-11-035-599-31
; Sequence 31, Application US/11035599
; Publication No. US20050158829A1
; GENERAL INFORMATION:
; APPLICANT: Fandl, James
; APPLICANT: Chen, Gang
; APPLICANT: Papadopoulos, Nicholas
; APPLICANT: Aldrich, Thomas F.
; TITLE OF INVENTION: Fusion Polypeptides Capable of
; TITLE OF INVENTION: Activating Receptors
; FILE REFERENCE: 1080A
; CURRENT APPLICATION NUMBER: US/11/035,599
; CURRENT FILING DATE: 2005-01-14
; PRIOR APPLICATION NUMBER: 60/536,968
; PRIOR FILING DATE: 2004-01-16
; NUMBER OF SEQ ID NOS: 53
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 31
; LENGTH: 730
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetic
US-11-035-599-31

Query Match 73.2%; Score 539.5; DB 6; Length 730;
Best Local Similarity 84.0%; Pred. No. 1.9e-40;
Matches 100; Conservative 11; Mismatches 5; Indels 3; Gaps 2;

Qy 20 VQLQESGPGLVKPSQSLSLCTCVTGYISITSGYAWNWIRQPPGNKLEWGWYISYGFTSYN 79
 |::|||::|||::|||::|||::|||::|||::|||::|||::|||::|||::|||::|||::|||::|||
Db 34 VKLEESGPGLVKPSQSLSLCTCVTGYISITSDYAWNWIROPFGNKLEWGWYINYSGITSYN 93
 |::|||::|||::|||::|||::|||::|||::|||::|||::|||::|||::|||::|||::|||::|||

Qy 80 PSLSRSIFTRDTSKNQFFLQNSVTSEDATYYCARWDYGTYYGF--DVWGQGTTVT 136
 |::|||::|||::|||::|||::|||::|||::|||::|||::|||::|||::|||::|||::|||::|||
Db 94 PSLKSRIISITRDTSKNQFFLQNSVTAEDATYYCARY-YGSSYNYGM DYWGQGSTVT 151
 |::|||::|||::|||::|||::|||::|||::|||::|||::|||::|||::|||::|||::|||::|||

RESULT 13

US-11-035-599-29
; Sequence 29, Application US/11035599
; Publication No. US20050158829A1
; GENERAL INFORMATION:
; APPLICANT: Fandl, James
; APPLICANT: Chen, Gang
; APPLICANT: Papadopoulos, Nicholas
; APPLICANT: Aldrich, Thomas F.
; TITLE OF INVENTION: Fusion Polypeptides Capable of
; TITLE OF INVENTION: Activating Receptors
; FILE REFERENCE: 1080A
; CURRENT APPLICATION NUMBER: US/11/035,599
; CURRENT FILING DATE: 2005-01-14
; PRIOR APPLICATION NUMBER: 60/536,968
; PRIOR FILING DATE: 2004-01-16
; NUMBER OF SEQ ID NOS: 53
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 29
; LENGTH: 761
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetic
US-11-035-599-29

Query Match 73.2%; Score 539.5; DB 6; Length 761;
Best Local Similarity 84.0%; Pred. No. 1.9e-40;
Matches 100; Conservative 11; Mismatches 5; Indels 3; Gaps 2;

Qy 20 VQLQESGPGLVKPSQSLSLCTCVTGYISITSGYAWNWIRQPPGNKLEWGWYISYGFTSYN 79
 |::|||::|||::|||::|||::|||::|||::|||::|||::|||::|||::|||::|||::|||::|||

RESULT 14

US-11-035-599-28
; Sequence 28, Application US/11035599
; Publication No. US20050158829A1
; GENERAL INFORMATION:
; APPLICANT: Fandl, James
; APPLICANT: Chen, Gang
; APPLICANT: Papadopoulos, Nicholas
; APPLICANT: Aldrich, Thomas F.
; TITLE OF INVENTION: Fusion Polypeptides Capable of
; TITLE OF INVENTION: Activating Receptors
; FILE REFERENCE: 1080A
; CURRENT APPLICATION NUMBER: US/11/035,599
; CURRENT FILING DATE: 2005-01-14
; PRIOR APPLICATION NUMBER: 60/536,968
; PRIOR FILING DATE: 2004-01-16
; NUMBER OF SEQ ID NOS: 53
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 28
; LENGTH: 762
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetic
US-11-035-599-28

Query Match 73.2%; Score 539.5; DB 6; Length 762;
Best Local Similarity 84.0%; Pred. No. 1.9e-40;
Matches 100; Conservative 11; Mismatches 5; Indels 3; Gaps 2;

Qy 20 VQLQESGPGLVKPSQSLSLCTCVTGYISITSGYAWNWIRQPPGNKLEWGWYISYGFTSYN 79
 |::|||::|||::|||::|||::|||::|||::|||::|||::|||::|||::|||::|||::|||::|||
Db 517 VKLEESGPGLVKPSQSLSLCTCVTGYISITSDYAWNWIROPFGNKLEWGWYINYSGITSYN 576
 |::|||::|||::|||::|||::|||::|||::|||::|||::|||::|||::|||::|||::|||::|||

RESULT 15

US-09-874-141-53
; Sequence 53, Application US/09874141
; Publication No. US20030012781A1
; GENERAL INFORMATION:
; APPLICANT: ANDERSON, DARRELL
; APPLICANT: PAN, LI-ZHEN
; APPLICANT: HANNA, NABIL
; APPLICANT: RASTETTER, WILLIAM H.
; APPLICANT: KLOETZER, WILLIAM S.
; TITLE OF INVENTION: NON-AGONISTIC ANTIBODIES TO HUMAN GP39, COMPOSITIONS
; TITLE OF INVENTION: CONTAINING, AND THERAPEUTIC USE THEREOF
; FILE REFERENCE: 037003-0280632
; CURRENT APPLICATION NUMBER: US/09/874,141
; CURRENT FILING DATE: 2001-06-06
; PRIOR APPLICATION NUMBER: 60/209,584
; PRIOR FILING DATE: 2000-06-06
; NUMBER OF SEQ ID NOS: 53
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 53
; LENGTH: 140
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-874-141-53

Query Match 72.7%; Score 535.5; DB 3; Length 140;
Best Local Similarity 76.5%; Pred. No. 7.6e-41;

```
Matches 104; Conservative 12; Mismatches 19; Indels 1; Gaps 1;
Qy 1 MRVLILLWLTAPGILSDVQLQESGPGLVKPSQSLSLTCSVTGYITSGYAWNWIRQPP 60
Db 1 MMVLSLLYLLTALPGFLSEVQLQESGPGSLVSPQTLTLTCSVTGDSITNGF-WIWIIRKPP 59
Qy 61 GNKLEWMGYISYSGFTSYNPSLRISFTRDTSKNOFFLQLNSVTSEDATYYCARWDYG 120
Db 60 GNKLEWMGYISYSGFTSYNPSLRISFTRDTSKNOFFLQLNSVTSEDATYYCARWDYG 119
Qy 121 TTYGYFDVMGQGTTVT 136
Db 120 RTPYYFDFWQGQTTLT 135
```

Search completed: May 19, 2006, 17:52:56
Job time : 134.841 secs

GenCore version 5.1.8
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OM protein - protein search, using sw model

Run on: May 19, 2006, 17:49:02 ; Search time 6.47619 Seconds
(without alignments)
44.858 Million cell updates/sec

Title: US-09-889-936A-6

Perfect score: 737

Sequence: 1 MRVLILLWLTAPPGLSDV.....WDYGTYYGYFDVWGQGTVT 136

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 21570 seqs, 2136119 residues

Total number of hits satisfying chosen parameters: 21570

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

Published Applications_AA_New.*
1: /EMC_Celerra_SID33/ptodata/2/pubpaa/US09_NEW_PUB.pep.*
2: /EMC_Celerra_SID33/ptodata/2/pubpaa/US06_NEW_PUB.pep.*
3: /EMC_Celerra_SID33/ptodata/2/pubpaa/US07_NEW_PUB.pep.*
4: /EMC_Celerra_SID33/ptodata/2/pubpaa/US08_NEW_PUB.pep.*
5: /EMC_Celerra_SID33/ptodata/2/pubpaa/PCT_NEW_PUB.pep.*
6: /EMC_Celerra_SID33/ptodata/2/pubpaa/US10_NEW_PUB.pep.*
7: /EMC_Celerra_SID33/ptodata/2/pubpaa/US11_NEW_PUB.pep.*
8: /EMC_Celerra_SID33/ptodata/2/pubpaa/US60_NEW_PUB.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	491	66.6	117	7	US-11-219-121-11
2	491	66.6	146	7	US-11-219-121-13
3	429	58.2	466	7	US-11-211-917-30
4	429	58.2	466	7	US-11-211-917-70
5	424	57.5	466	7	US-11-211-917-86
6	419.5	56.9	118	7	US-11-211-917-142
7	419	56.9	118	6	US-10-981-300-51
8	418	56.7	118	6	US-10-981-300-54
9	418	56.7	443	6	US-11-211-917-20
10	417.5	56.6	118	7	US-11-211-917-109
11	412	55.9	121	7	US-11-211-917-26
12	412	55.9	121	7	US-11-211-917-98
13	410	55.6	121	7	US-11-211-917-66
14	409.5	55.6	115	6	US-10-981-300-53
15	407	55.2	121	7	US-11-211-917-82
16	399	54.1	451	7	US-11-254-182-43
17	398	54.0	451	7	US-11-254-182-41
18	398	54.0	451	7	US-11-254-182-42
19	396	53.7	286	7	US-11-154-103-8
20	396	53.7	464	7	US-11-211-917-22
21	393	53.3	118	6	US-10-981-300-52
22	393	53.3	180	6	US-10-981-300-4
23	390	52.9	447	7	US-11-219-121-32
24	386.5	52.4	120	7	US-11-211-917-108
25	379	51.4	119	7	US-11-211-917-18

26 376 51.0 117 7 US-11-219-121-26 Sequence 26, Appl
27 376 51.0 447 7 US-11-219-121-30 Sequence 30, Appl
28 373.5 50.7 118 6 US-10-983-104-8 Sequence 8, Appl
29 351 47.6 121 7 US-11-219-563-84 Sequence 84, Appl
30 351 47.6 121 7 US-11-219-563-89 Sequence 89, Appl
31 351 47.6 121 7 US-11-219-563-90 Sequence 90, Appl
32 342.5 46.5 471 7 US-11-106-762-25 Sequence 25, Appl
33 342.5 46.5 471 7 US-11-106-762-27 Sequence 27, Appl
34 340.5 46.2 120 7 US-11-254-679-15 Sequence 15, Appl
35 336 45.6 123 7 US-11-254-182-36 Sequence 36, Appl
36 335 45.5 123 7 US-11-254-182-34 Sequence 34, Appl
37 329 44.6 123 7 US-11-211-917-117 Sequence 117, Appl
38 327.5 44.4 120 7 US-11-230-593A-31 Sequence 31, Appl
39 325.5 44.2 291 7 US-11-154-103-10 Sequence 10, Appl
40 325 44.1 123 7 US-11-211-917-116 Sequence 116, Appl
41 325 44.1 470 7 US-11-211-917-78 Sequence 78, Appl
42 324 44.0 123 7 US-11-211-917-115 Sequence 115, Appl
43 322.5 43.8 452 7 US-11-106-762-34 Sequence 34, Appl
44 322.5 43.8 452 7 US-11-106-762-36 Sequence 36, Appl
45 321.5 43.6 120 7 US-11-230-593A-33 Sequence 33, Appl

ALIGNMENTS

RESULT 1

US-11-219-121-11

; Sequence 11, Application US/11219121

; Publication No. US20060093601A1

; GENERAL INFORMATION:

; APPLICANT: Pong, Sherman

; APPLICANT: Dennis Mark S.

; TITLE OF INVENTION: HUMANIZED ANTI-BETA7 ANTAGONISTS AND USES THEREFOR

; FILE REFERENCE: P2159R1

; CURRENT APPLICATION NUMBER: US/11/219,121

; PRIOR FILING DATE: 2005-09-02

; PRIOR APPLICATION NUMBER: US 60/607,377

; PRIOR FILING DATE: 2004-09-03

; NUMBER OF SEQ ID NOS: 68

; SEQ ID NO 11

; LENGTH: 117

; TYPE: PRT

; ORGANISM: Artificial sequence

; FEATURE:

; OTHER INFORMATION: sequence is synthesized

US-11-219-121-11

Query Match 66.6%; Score 491; DB 7; Length 117;

Best Local Similarity 79.7%; Pred. No. 6.7e-31;

Matches 94; Conservative 8; Mismatches 12; Indels 4; Gaps 2;

QY 19 DVQLQESGGLVKPQSLSLTCSVTGYTSYGVAMNWIQFPGNKLWVGYSYSGTYSY 78

:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||

Db 1 EVQLQESGGLVKPQSLSLTCSVTGYTFITNNY-WGWIKRFPGNKLWVGYSYSGTYSY 59

:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||

QY 79 NPSLRSRISFTDTSKNQFFLQNSVTSBTDATYYCARWDYGTYYFDVWGQGTVT 136

:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||

Db 60 NPSLRSRISFTDTSKNQFFLQNSVTSBTDATYYCAMTG---SSGYFDVWGQGTMT 114

:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||

RESULT 2

US-11-219-121-13

; Sequence 13, Application US/11219121

; Publication No. US20060093601A1

; GENERAL INFORMATION:

; APPLICANT: Pong, Sherman

; APPLICANT: Dennis Mark S.

; TITLE OF INVENTION: HUMANIZED ANTI-BETA7 ANTAGONISTS AND USES THEREFOR

; FILE REFERENCE: P2159R1

; CURRENT APPLICATION NUMBER: US/11/219,121

; PRIOR FILING DATE: 2005-09-02

; PRIOR APPLICATION NUMBER: US 60/607,377

; NUMBER OF SEQ ID NOS: 68

; SEQ ID NO 11

; LENGTH: 117

; TYPE: PRT

; ORGANISM: Artificial sequence

; FEATURE:

; OTHER INFORMATION: sequence is synthesized

```
; NUMBER OF SEQ ID NOS: 68
; SEQ ID NO 13
; LENGTH: 146
; TYPE: PRT
; ORGANISM: Artificial sequence
; FEATURE:
; OTHER INFORMATION: sequence is synthesized
US-11-219-121-13

Query Match
Best Local Similarity 66.6%; Score 491; DB 7; Length 146;
Matches 94; Conservative 8; Mismatches 12; Indels 4; Gaps 2;

QY 19 DVLOQSGPGLVKPSQSLTSCVTGYSITSGYANNWIRQPGNKLWNGYISYSGFTSY 78
Db 1 EVOLQSGPGLVKPSQSLTSCVTGFTTNNY-WGWIIRKFGNKMWMWYISYSGSTSY 59

QY 79 NPSLRISIRTRDTSKNQFFLQNSVTSBTDATYYCARWDYGTYYGVFVWVGQGTVT 136
Db 60 NPSLKRISIRTRDTSKNQFFLQNSVTTEDATYYCAMTG---SSGYFDWFGPGTMTV 114

RESULT 3
US-11-211-917-30
; Sequence 30, Application US/11211917
; Publication No. US20060093600A1
; GENERAL INFORMATION:
; APPLICANT: BEDIAN, VAHE
; APPLICANT: GLADUE, RONALD P.
; APPLICANT: CORVALAN, JOSE
; APPLICANT: JIA, XIAO-CHI
; APPLICANT: FENG, XIAO
; TITLE OF INVENTION: ANTIBODIES TO CD40
; FILE REFERENCE: ABX-PF/3 US
; CURRENT APPLICATION NUMBER: US/11/211,917
; PRIOR FILING DATE: 2005-08-25
; PRIOR FILING DATE: 2002-11-08
; PRIOR APPLICATION NUMBER: 60/348,980
; PRIOR FILING DATE: 2001-11-09
; NUMBER OF SEQ ID NOS: 147
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 30
; LENGTH: 466
; TYPE: PRT
; ORGANISM: Homo sapiens
US-11-211-917-30

Query Match
Best Local Similarity 58.2%; Score 429; DB 7; Length 466;
Matches 87; Conservative 15; Mismatches 27; Indels 6; Gaps 4;

QY 7 LWLF---TAPP-GILSDVOLQSGPGLVKPQSLSLTCSVTGYSITSGYANNWIRQPGN 62
Db 4 LWFFLLLVAAPRWVLSQVLOQSGPGLVKPSETLSLTCTVSGGSI-RGYNWSWIRQPGK 62

QY 63 KLEWMGYISYSGFTSYNPSLRISIRTRDTSKNQFFLQNSVTSBTDATYYCARWD--YG 120
Db 63 GLEWIGYIYSGSTNYNPSLSKSRVTISVDTSKNQPSLKLSSVTAADTAVYYCARGGLYG 122

QY 121 TYGYFDVWVGQGTVT 136
Db 123 -DYGWFAFWGQGTIVT 137

RESULT 5
US-11-211-917-86
; Sequence 86, Application US/11211917
; Publication No. US20060093600A1
; GENERAL INFORMATION:
; APPLICANT: BEDIAN, VAHE
; APPLICANT: GLADUE, RONALD P.
; APPLICANT: CORVALAN, JOSE
; APPLICANT: JIA, XIAO-CHI
; APPLICANT: FENG, XIAO
; TITLE OF INVENTION: ANTIBODIES TO CD40
; FILE REFERENCE: ABX-PF/3 US
; CURRENT APPLICATION NUMBER: US/11/211,917
; CURRENT FILING DATE: 2005-08-25
; PRIOR FILING DATE: 2005-08-25
; PRIOR FILING DATE: 2002-11-08
; PRIOR APPLICATION NUMBER: 60/348,980
; PRIOR FILING DATE: 2001-11-09
; NUMBER OF SEQ ID NOS: 147
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 86
; LENGTH: 466
; TYPE: PRT
; ORGANISM: Homo sapiens
US-11-211-917-86

Query Match
Best Local Similarity 57.5%; Score 424; DB 7; Length 466;
Matches 88; Conservative 16; Mismatches 16; Indels 8; Gaps 5;

QY 7 LWLF---TAPP-GILSDVOLQSGPGLVKPQSLSLTCSVTGYSITSGYANNWIRQPGN 62
Db 4 LWFFLLLVAAPRWVLSQVLOQSGPGLVKPSETLSLTCTVSGGSI-RGYNWSWIRQPGK 62

QY 63 KLEWMGYISYSGFTSYNPSLRISIRTRDTSKNQFFLQNSVTSBTDATYYCARWD--YG 120
Db 63 GLEWIGYIYSGSTNYNPSLSKSRVTISVDTSKNQPSLKLSSVTAADTAVYYCARGGLYG 122
```

Qy 121 TTYGYFDVWGQTTVT 136
 ||:| |||||
 Db 123 -DYGWEAPWGQTLVT 137

```

RESULT 6
US-11-211-917-142
; Sequence 142, Application US/11211917
; Publication No. US20060093600A1
; GENERAL INFORMATION:
; APPLICANT: BEDIAN, VAHE
; APPLICANT: GLADUE, RONALD P.
; APPLICANT: CORVALAN, JOSE
; APPLICANT: JIA, XIAO-CHI
; APPLICANT: FENG, XIAO
; TITLE OF INVENTION: ANTIBODIES TO CD40
; FILE REFERENCE: AEX-PF/3 US
; CURRENT APPLICATION NUMBER: US/11/211,917
; CURRENT FILING DATE: 2005-08-25
; PRIOR APPLICATION NUMBER: US/10/292,088
; PRIOR FILING DATE: 2002-11-08
; PRIOR APPLICATION NUMBER: 60/348,980
; PRIOR FILING DATE: 2001-11-09
; NUMBER OF SEQ ID NOS: 147
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 142
; LENGTH: 118
; TYPE: PRT
; ORGANISM: Homo sapiens
US-11-211-917-142

```

		Query Match	56.9%; Score 419.5; DB 7; Length 118;
		Best Local Similarity	70.1%; Pred. No. 1.3e-25;
		Matches	82; Conservative 16; Mismatches 16; Indels 3; Gaps 3;
Qy	20	VQLQESPGGLVKPSQSLLTCSVTGYITSGYANNWIROPCKNLEHWGIIISYGFTSYN	79
		: : : :	
		: : : :	
		: : : :	
Db	2	VQLQESPGGLVKPSETLSLTCVSSGGISS--YYMSWIRQPPKGKLEWIGIYYISGSNTYN	60
		: : : :	
		: : : :	
		: : : :	
Qy	80	PSLRSRISFTRDTSKNOFFQLNSVTSEDATYYICARDYCTTTGYFDVWGQTHTV	136
		: : : :	
		: : : :	
		: : : :	
Db	61	PSLKSRVTISVDTSKNQFSKLKSVAADTAIVVYCAR-DYGDYNWFDPWGOGLTVT	115
		: : : :	
		: : : :	
		: : : :	

```

RESULT 7
US-10-981-300-51
; Sequence 51, Application US/10981300
; Publication No. US2006009359A1
; GENERAL INFORMATION:
; APPLICANT: GIORGIO SENALDI
; APPLICANT: GADI GAZIT-BORNSTEIN
; TITLE OF INVENTION: ANTI-PROPERDIN ANTIBODIES, AND METHODS
; TITLE OF INVENTION: FOR MAKING AND USING THE SAME
; FILE REFERENCE: ABGX-005
; CURRENT APPLICATION NUMBER: US/10/981,300
; CURRENT FILING DATE: 2004-11-03
; NUMBER OF SEQ ID NOS: 71
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 51
; LENGTH: 118
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-981-300-51

```

Query Match	56.9%	Score	419	DB	6	Length	118
Best Local Similarity	69.5%	Pred. No.	1.4e-25				
Matches	8	Conservative	13	Mismatches	17	Indels	6
Gaps	2						
Qy	20	VQLQESGFLVKPQSILTCSVTGYGITS	-GYAANWIRPPGKNLEMGVYISGFTSY	78			
Db	2	VQLQESGFLVKPQSILTCSVTGGYISGYYWIRPPGKLEWIGYIYSGTYY	61				
Qv	79	NPLRSRISRTDRTSKNOFFLQNLNSVTSEDTATYYCARWDYGTYYGFDVWGCGTIVT	136				

```

|||||::: : ||||| |::|: ||| |||||
62 NPSLSRVITSDTSKNQFSLKSSVTAADAVYICAR-----TGDYPDWGGTLVT 114

Db

RESULT 8
US-10-981-300-54
; Sequence 54, Application US/10981300
; Publication No. US20060093599A1
; GENERAL INFORMATION:
; APPLICANT: GIORGIO SENALDI
; APPLICANT: GADI GAZIT-BORNSTEIN
; TITLE OF INVENTION: ANTI-PROPERDIN ANTIBODIES, AND METHODS
; TITLE OF INVENTION: FOR MAKING AND USING THE SAME
; FILE REFERENCE: ABGX-005
; CURRENT APPLICATION NUMBER: US/10/981,300
; CURRENT FILING DATE: 2004-11-03
; NUMBER OF SEQ ID NOS: 71
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 54
; LENGTH: 118
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-981-300-54
```

[illegible]

```

RESULT 9
US-10-981-300-20
; Sequence 20, Application US/10981300
; Publication No. US20060093599A1
; GENERAL INFORMATION:
; APPLICANT: GIORGIO SENALDI
; APPLICANT: GADI GAZIT-BORNSTEIN
; TITLE OF INVENTION: ANTI-PROPERDIN ANTIBODIES, AND METHODS
; TITLE OF INVENTION: FOR MAKING AND USING THE SAME
; FILE REFERENCE: ABGX-005
; CURRENT APPLICATION NUMBER: US/10/981.300
; CURRENT FILING DATE: 2004-11-03
; NUMBER OF SEQ ID NOS: 71
; SOFTWARE: FaastSEQ for Windows Version 4.0
; SEQ ID NO 20
; LENGTH: 443
; TYPE: PRT
; ORGANISM: homo sapien
US-10-981-300-20

```

	Query Match	56.7%;	Score 418;	DB 6;	Length 443;	
	Best Local Similarity	68.4%;	Pred.No. 5.3e-25;			
	Matches	80;	Conservative	16;	Mismatches	17; Indels 4; Gaps 2;
Qy	20	VQLQESGPGLVKPSQSLSLCTSVGTGSYITSGYAWNWIROPGNKLEHMGVIISYGFTSYN	79			
		:::::::::::::::::::::				
Db	2	VQLQESGPGLVKPSLSLCTSVGGSI-SIYYMSWIRQPPGKGLEWIGVITYSGSTNYN	60			
		:::::::::::::::::::::				
Qy	80	PSLSRISITRDTSKNQOFFLQLNSVTSEDATYYCARWDYTGTTYGYEDVWGQGTTVT	136			
		:::::::::::::::::::::				
Db	61	PSLKSRTVTSVDTSKNQFSLKLSVTAADPAVYCAVNTGDA---FDIWGQGTMTVT	114			
		:::::::::::::::::::::				

RESULT 10
US-11-211-917-109
; Sequence 109, Application US/11211917

```

; Publication No. US20060093600A1
; GENERAL INFORMATION:
; APPLICANT: BEDIAN, VAHE
; APPLICANT: GLADUE, RONALD P.
; APPLICANT: CORVALAN, JOSE
; APPLICANT: JIA, XIAO-CHI
; APPLICANT: FENG, XIAO
; TITLE OF INVENTION: ANTIBODIES TO CD40
; FILE REFERENCE: ABX-PF/3 US
; CURRENT APPLICATION NUMBER: US/11/211,917
; CURRENT FILING DATE: 2005-08-25
; PRIOR APPLICATION NUMBER: US/10/292,088
; PRIOR FILING DATE: 2002-11-08
; PRIOR APPLICATION NUMBER: 60/348,980
; PRIOR FILING DATE: 2001-11-09
; NUMBER OF SEQ ID NOS: 147
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 109
; LENGTH: 118
; TYPE: PRT
; ORGANISM: Homo sapiens
US-11-211-917-109

Query Match      56.6%; Score 417.5; DB 7; Length 118;
Best Local Similarity 70.1%; Pred. No. 1.8e-25;
Matches 82; Conservative 15; Mismatches 17; Indels 3; Gaps 3;

QY 20 VOLQESGGLVKPQSLSLTCSTGYTSGYANWIRQFPGNKLEWMGYISYSGFTSYN 79
DB 2 VOLQESGGLVKPSETLSLTCVSGSIRS-YWWSWIRQPGKGLEWIGYIYSGSTNYN 60

QY 80 PSLRSRISFTRDTSKNQFLLQNSVTSEDATYYCARWDYGTYYGVDFVWGQGTVT 136
DB 61 PSLKSRVTISVDTSKNQFSLKLSVTAADTAVYYCAR-DYGN-SYFDYWGQGTTLV 115

RESULT 11
US-11-211-917-26
; Sequence 26, Application US/11211917
; Publication No. US20060093600A1
; GENERAL INFORMATION:
; APPLICANT: BEDIAN, VAHE
; APPLICANT: GLADUE, RONALD P.
; APPLICANT: CORVALAN, JOSE
; APPLICANT: JIA, XIAO-CHI
; APPLICANT: FENG, XIAO
; TITLE OF INVENTION: ANTIBODIES TO CD40
; FILE REFERENCE: ABX-PF/3 US
; CURRENT APPLICATION NUMBER: US/11/211,917
; CURRENT FILING DATE: 2005-08-25
; PRIOR APPLICATION NUMBER: US/10/292,088
; PRIOR FILING DATE: 2002-11-08
; PRIOR APPLICATION NUMBER: 60/348,980
; PRIOR FILING DATE: 2001-11-09
; NUMBER OF SEQ ID NOS: 147
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 26
; LENGTH: 121
; TYPE: PRT
; ORGANISM: Homo sapiens
US-11-211-917-26

Query Match      55.9%; Score 412; DB 7; Length 121;
Best Local Similarity 67.8%; Pred. No. 4.6e-25;
Matches 80; Conservative 14; Mismatches 22; Indels 2; Gaps 2;

QY 20 VOLQESGGLVKPQSLSLTCSTGYTSGYANWIRQFPGNKLEWMGYISYSGFTSYN 79
DB 2 VOLQESGGLVKPSETLSLTCVSGSIRS-YWWSWIRQPGKGLEWIGYIYSGSTNYN 60

QY 80 PSLRSRISFTRDTSKNQFLLQNSVTSEDATYYCARWDYGTYYGVDFVWGQGTVT 136
DB 61 PSLKSRVTISVDTSKNQFSLKLSVTAADTAVYYCAR-DYGN-SYFDYWGQGTTLV 115

RESULT 12
US-11-211-917-98
; Sequence 98, Application US/11211917
; Publication No. US20060093600A1
; GENERAL INFORMATION:
; APPLICANT: BEDIAN, VAHE
; APPLICANT: GLADUE, RONALD P.
; APPLICANT: CORVALAN, JOSE
; APPLICANT: JIA, XIAO-CHI
; APPLICANT: FENG, XIAO
; TITLE OF INVENTION: ANTIBODIES TO CD40
; FILE REFERENCE: ABX-PF/3 US
; CURRENT APPLICATION NUMBER: US/11/211,917
; CURRENT FILING DATE: 2005-08-25
; PRIOR APPLICATION NUMBER: US/10/292,088
; PRIOR FILING DATE: 2002-11-08
; PRIOR APPLICATION NUMBER: 60/348,980
; PRIOR FILING DATE: 2001-11-09
; NUMBER OF SEQ ID NOS: 147
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 98
; LENGTH: 121
; TYPE: PRT
; ORGANISM: Homo sapiens
US-11-211-917-98

Query Match      55.9%; Score 412; DB 7; Length 121;
Best Local Similarity 68.9%; Pred. No. 4.6e-25;
Matches 82; Conservative 14; Mismatches 19; Indels 4; Gaps 3;

QY 20 VOLQESGGLVKPQSLSLTCSTGYTSGYANWIRQFPGNKLEWMGYISYSGFTSYN 79
DB 2 VOLQESGGLVKPSETLSLTCVSGGSI-RGYYSWIRQPGKGLEWIGYIYSGSTNYN 60

QY 80 PSLRSRISFTRDTSKNQFLLQNSVTSEDATYYCARWDYGTYYGVDFVWGQGTVT 136
DB 61 PSLKSRVTISVDTSKNQFSLKLSVTAADTAVYYCAR-KGGLYG-DYGFAPWGQGTTLV 118

RESULT 13
US-11-211-917-66
; Sequence 66, Application US/11211917
; Publication No. US20060093600A1
; GENERAL INFORMATION:
; APPLICANT: BEDIAN, VAHE
; APPLICANT: GLADUE, RONALD P.
; APPLICANT: CORVALAN, JOSE
; APPLICANT: JIA, XIAO-CHI
; APPLICANT: FENG, XIAO
; TITLE OF INVENTION: ANTIBODIES TO CD40
; FILE REFERENCE: ABX-PF/3 US
; CURRENT APPLICATION NUMBER: US/11/211,917
; CURRENT FILING DATE: 2005-08-25
; PRIOR APPLICATION NUMBER: US/10/292,088
; PRIOR FILING DATE: 2002-11-08
; PRIOR APPLICATION NUMBER: 60/348,980
; PRIOR FILING DATE: 2001-11-09
; NUMBER OF SEQ ID NOS: 147
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 66
; LENGTH: 121
; TYPE: PRT
; ORGANISM: Homo sapiens
US-11-211-917-66

Query Match      55.6%; Score 410; DB 7; Length 121;
Best Local Similarity 68.9%; Pred. No. 6.5e-25;
Matches 82; Conservative 13; Mismatches 20; Indels 4; Gaps 3;

QY 20 VOLQESGGLVKPQSLSLTCSTGYTSGYANWIRQFPGNKLEWMGYISYSGFTSYN 79
DB 2 VOLQESGGLVKPSETLSLTCVSGSIRS-YWWSWIRQPGKGLEWIGYIYSGSTNYN 60
```

Db 2 VOLQESGPGLVKPSDLSLTCTVSGGSI-RGYWWSWIRPPGKGLEWIGYIYSGSTNYN 60
Qy 80 PSLRSRISFTRDTSKNQFFLQLNSVTSEDTATYYCARWD--YCTTYGYFDVWVGQGTTVT 136
Db 61 PSLKSRVTISVDTSKNQFSLKLSVTAADTAVYYCARKGGLYG-DYGFAPWVGQGTTLVT 118

RESULT 14
US-10-981-300-53
; Sequence 53, Application US/10981300
; Publication No. US20060093599A1
; GENERAL INFORMATION:
; APPLICANT: GIORGIO SENALDI
; APPLICANT: GADI GAZIT-BORNSTEIN
; TITLE OF INVENTION: ANTI-PROPERDIN ANTIBODIES, AND METHODS
; TITLE OF INVENTION: FOR MAKING AND USING THE SAME
; FILE REFERENCE: ABGX-005
; CURRENT APPLICATION NUMBER: US/10/981,300
; CURRENT FILING DATE: 2004-11-03
; NUMBER OF SEQ ID NOS: 71
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 53
; LENGTH: 115
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-981-300-53

Query Match 55.6%; Score 409.5; DB 6; Length 115;
Best Local Similarity 67.5%; Pred. No. 6.7e-25;
Matches 79; Conservative 17; Mismatches 14; Indels 7; Gaps 3;
Qy 20 VOLQESGPGLVKPSDLSLTCTVSGGSI-RGYWWSWIRPPGKGLEWIGYIYSGSTNYN 79
Db 2 VOLQESGPGLVKPSDLSLTCTVSGGSI-RGYWWSWIRPPGKGLEWIGYIYSGSTNYN 60
Qy 80 PSLRSRISFTRDTSKNQFFLQLNSVTSEDTATYYCARWDYCTTYGYFDVWVGQGTTVT 136
Db 61 PSLKSRVTISVDTSKNQFSLKLSVTAADTAVYYCA-WNYA-----FDWVGQGTWVT 111

RESULT 15
US-11-211-917-82
; Sequence 82, Application US/11211917
; Publication No. US20060093600A1
; GENERAL INFORMATION:
; APPLICANT: BEDIAN, VAHE
; APPLICANT: GLADUE, RONALD P.
; APPLICANT: CORVALAN, JOSE
; APPLICANT: JIA, XIAO-CHI
; APPLICANT: FENG, XIAO
; TITLE OF INVENTION: ANTIBODIES TO CD40
; CURRENT APPLICATION NUMBER: US/11/211,917
; CURRENT FILING DATE: 2005-08-25
; PRIOR APPLICATION NUMBER: US/10/292,088
; PRIOR FILING DATE: 2002-11-08
; PRIOR APPLICATION NUMBER: 60/348,980
; PRIOR FILING DATE: 2001-11-09
; NUMBER OF SEQ ID NOS: 147
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 82
; LENGTH: 121
; TYPE: PRT
; ORGANISM: Homo sapiens
US-11-211-917-82

Query Match 55.2%; Score 407; DB 7; Length 121;
Best Local Similarity 68.1%; Pred. No. 1.1e-24;
Matches 81; Conservative 15; Mismatches 19; Indels 4; Gaps 3;
Qy 20 VOLQESGPGLVKPSDLSLTCTVSGGSI-RGYWWSWIRPPGKGLEWIGYIYSGSTNYN 79
Db 2 VOLQESGPGLVKPSDLSLTCTVSGGSI-RGYWWSWIRPPGKGLEWIGYIYSGSTNYN 60

Qy 80 PSLRSRISFTRDTSKNQFFLQLNSVTSEDTATYYCARWD--YCTTYGYFDVWVGQGTTVT 136
Db 61 PSLKSRVTISVDTSKNQFSLKLSVTAADTAVYYCARKGGLYG-DYGFAPWVGQGTTLVT 118
Search completed: May 19, 2006, 17:53:13
Job time : 7.47619 secs

GenCore version 5.1.8
Copyright (c) 1993 - 2006 Bioceleration Ltd.
OM*protein - protein search, using sw model
Run on: May 19, 2006, 17:34:57 ; Search time 135.333 Seconds
(without alignments)
391.900 Million cell updates/sec

Title: US-09-889-936A-8
Perfect score: 606
Sequence: 1 SRGDIVMTQSPSSLSVSAGE.....QNDHIYPTFGGKLEIK 116
Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5
Searched: 2589679 seqs, 457216429 residues
Total number of hits satisfying chosen parameters: 2589679

Minimum DB seq length: 0
Maximum DB seq length: 2000000000
Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : A_Geneseq_8.*
1: Geneseq1980s.*
2: Geneseq1990s.*
3: Geneseq2000s.*
4: Geneseq2001s.*
5: Geneseq2002s.*
6: Geneseq2003as.*
7: Geneseq2003bs.*
8: Geneseq2004s.*
9: Geneseq2005s.*
10: Geneseq2006s.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	606	100.0	116	3 AAB15673	Aab15673 Murine 5B
2	545	89.9	113	7 ADD94117	Add94117 Mouse HUI
3	545	89.9	113	9 ADV66167	Adv66167 Human Epc
4	545	89.9	113	9 ADZ83525	Adz83525 AntiEpCam
5	545	89.9	248	2 AAY17960	Aay17960 Mouse scf
6	545	89.9	497	9 ADZ83445	Adz83445 CD3 specf
7	545	89.9	500	9 ADV66137	Adv66137 Anti-CD3-
8	545	89.9	503	9 ADV66133	Adv66133 Anti-CD3-
9	545	89.9	503	9 ADV66135	Adv66135 Anti-CD3-
10	545	89.9	515	9 ADZ83436	Adz83436 Deimmuniz
11	545	89.9	521	9 ADV66116	Adv66116 Anti-CD3-
12	540	89.1	114	4 AAB62864	Aab62864 Anti-SAF-
13	536	88.4	113	2 AAR38603	Aar38603 MCPC ligh
14	536	88.4	113	2 AAR68742	Aar68742 Mab MCPG6
15	536	88.4	113	2 AAW58483	Aaw58483 Murine MC
16	536	88.4	113	8 ADI01145	Adi01145 Murine MC
17	536	88.4	115	2 AAR52036	Aar52036 Light cha
18	536	88.4	115	8 ADO32152	Aod32152 Mouse ant
19	536	88.4	118	9 AED64796	Aed64796 Murine an
20	536	88.4	220	2 AAR53802	Aar53802 FAB light
21	535	88.3	113	2 AAW42468	Aaw42468 Fab15 lig
22	534	88.1	116	1 AAR80460	Aar80460 Sequence
23	534	88.1	277	2 AAR39336	Aar39336 scfv frag

24	532	87.8	113	2 AAR54102	Aar54102 Humanised
25	532	87.8	113	2 AAW42467	Aaw42467 Fab2 ligh
26	528	87.1	113	2 AAR90834	Aar90834 17F6 ligh
27	526	86.8	113	2 AAR98479	Aar98479 Mab 2B6 1
28	526	86.8	113	2 AAW42452	Aaw42452 Mouse ant
29	526	86.8	679	10 AEF80923	Aef80923 Staphyloc
30	525	86.6	482	2 AAY06915	Aay06915 Amino aci
31	523	86.3	118	7 ADD13796	Add13796 Plasmid p
32	521	86.0	113	2 AAR90839	Aar90839 14G1 ligh
33	520	85.8	263	7 ADG32320	Adg32320 Mouse scf
34	518	85.5	115	3 AAB28395	Aab28395 Anti-VEGF
35	518	85.5	115	5 AAU77947	Aau77947 Variable
36	516	85.1	113	6 ABO10744	Abo10744 Variable
37	516	85.1	113	6 ABO10756	Abo10756 Variable
38	516	85.1	113	6 ABR44700	Abr44700 Murine Mu
39	516	85.1	113	6 ABR44688	Abr44688 Murine Mu
40	516	85.1	113	8 ADQ090822	Adq090822 Kabat sub
41	516	85.1	113	8 ADU67950	Adu67950 Mouse Kab
42	516	85.1	113	8 ADU67970	Adu67970 Mouse Kab
43	516	85.1	113	9 AED41851	Aed41851 Mouse pro
44	516	85.1	113	9 AED41871	Aed41871 Mouse pro
45	513	84.7	113	9 ADV66175	Adv66175 Human Epc

ALIGNMENTS

RESULT 1
AAB15673
ID AAB15673 standard; protein; 116 AA.
XX
AC AAB15673;
XX
DT 08-JAN-2001 (first entry)
XX
DE Murine 5B3 antibody light chain variable region.
XX
KW Mouse; 5B3 antibody; IgG1; piezoelectric immunoassay;
KW small molecule explosive detection; 2,4,6-trinitrotoluene; TNT.
OS Mus sp.
XX
PN WO200043774-A2.
XX
PD 27-JUL-2000.
XX
PF 25-JAN-2000; 2000WO-IL000048.
XX
PR 25-JAN-1999; 99IL-00128212.
XX
PA (YISS) YISSUM RES & DEV CO.
PA (VEDA) YEDA RES & DEV CO LTD.
XX
PI Willner I, Eshhar Z;
XX
DR WPI; 2000-524259/47.
XX
DR N-PSDB; AAA74605.
XX
PT Apparatus for detecting small molecules, especially explosives comprises
PT a piezoelectric crystal.
XX
PS Disclosure; Fig 3B; 90pp; English.
XX
CC The present sequence is the light chain variable region of 5B3 antibody.
CC The cDNA encoding this sequence was obtained from total RNA extracted
CC from a 5B3 hybridoma by RT-PCR. 5B3 is an IgG1 antibody derived from a
CC TNP-KLH immunised mouse. Its binding to TNP or DNS antigen can be blocked
CC by very low amounts of TNT and it can therefore be used in a method for
CC detecting small assayed explosive molecules. Molecules are detected using
CC a piezoelectric sensor. Piezoelectric immunoassaying in liquid phase
CC allows stationary and flow analysis of an aqueous sample. The method is
CC sufficiently sensitive for detection of low molecular weight molecules

SQ	Sequence 116 AA;	
Query Match	100.0%; Score 606; DB 3; Length 116;	
Best Local Similarity	100.0%; Pred. No. 2.4e-43;	
Matches 116; Conservative	0; Mismatches 0; Indels 0; Gaps 0;	
QY	1 SRGDIWMTQSPSSLSVSAAGEKVTMSCKSSQSLNSRNQKNYLAWYQKPGQPPKLLIYG 60	
DB	1 SRGDIWMTQSPSSLSVSAAGEKVTMSCKSSQSLNSRNQKNYLAWYQKPGQPPKLLIYG 60	
QY	61 FIRDSGVDRFTGSGSGTDFLTITSSVQAEIDLAVYYCQNDHIYPYTFGGGKLEIK 116	
DB	61 FIRDSGVDRFTGSGSGTDFLTITSSVQAEIDLAVYYCQNDHIYPYTFGGGKLEIK 116	
RESULT 2		
ADD94117		
ID	ADD94117 standard; protein; 113 AA.	
AC	ADD94117;	
XX		
DT	29-JAN-2004 (first entry)	
XX		
DE	Mouse HUIV26 variable region light chain partial amino acid sequence.	
XX		
KW	grafted antibody; complementarity determining region; CDR; light CDR;	
KW	heavy CDR; cryptic collagen epitope; solid tumour;	
KW	new blood vessel growth; angiogenesis; tumour growth; cytostatic;	
KW	collagen agonist; collagen antagonist; cancer metastasis;	
KW	anti-cryptic collagen; antibody; HUIV26; variable region light chain;	
KW	mouse; murine.	
XX		
OS	Mus musculus.	
XX		
PN	WO2003046204-A2.	
XX		
PD	05-JUN-2003.	
XX		
PF	26-NOV-2002; 2002WO-US038147.	
XX		
PR	26-NOV-2001; 2001US-00995529.	
PR	06-DEC-2001; 2001US-00011250.	
XX		
PA	(CELL-) CELL MATRIX INC.	
XX		
PI	Watking JD, Huse WD, Tang Y, Broek D, Brooks PC;	
XX		
DR	WPI; 2003-513649/48.	
DR	N-PSDB; ADD94116.	
XX		
PT	New cryptic collagen antibody with one or more complementarity	
PT	determining regions, useful for diagnosing and treating disorders	
PT	associated with angiogenesis, tumor growth and/or cancer metastasis.	
PS	Example 1; SEQ ID NO 2; 232pp; English.	
XX		
CC	This invention relates to a novel grafted antibody or its functional	
CC	fragment comprising one or more complementarity determining regions	
CC	(CDRs) of a defined light CDR and a heavy CDR with at least one amino	
CC	acid (aa) substitution where the antibody has specific binding activity	
CC	for a cryptic collagen epitope. The growth of all solid tumours requires	
CC	new blood vessel growth, angiogenesis, inhibition of which is an approach	
CC	to limiting tumour growth. The invention may allow development of	
CC	therapeutics with a cytostatic activity as a collagen agonist or	
CC	antagonist. The invention is useful for diagnosing and treating disorders	
CC	associated with angiogenesis, tumour growth and/or cancer metastasis. The	
CC	present sequence is the partial amino acid sequence of the mouse anti-	
CC	cryptic collagen site antibody HUIV26 variable region light chain used	
CC	during the creation of the antibody of the invention.	
XX		
SQ	Sequence 113 AA;	
Query Match	89.9%; Score 545; DB 7; Length 113;	
Best Local Similarity	89.9%; Pred. No. 3.1e-38;	
Matches 104; Conservative	4; Mismatches 5; Indels 0; Gaps 0;	
QY	4 DIVMTQSPSSLSVSAAGEKVTMSCKSSQSLNSRNQKNYLAWYQKPGQPPKLLIYG 63	
DB	1 ELVMTQSPSSLSVSAAGEKVTMSCKSSQSLNSRNQKNYLAWYQKPGQPPKLLIYG 60	
QY	64 DSGVPDRFTGSGSGTDFLTITSSVQAEIDLAVYYCQNDHIYPYTFGGGKLEIK 116	
DB	61 ESGVPDRFTGSGSGTDFLTITSSVQAEIDLAVYYCQNDHSYPYTFGGGKLEIK 113	
Query Match	89.9%; Score 545; DB 9; Length 113;	
Best Local Similarity	92.0%; Pred. No. 3.1e-38;	
Matches 104; Conservative	4; Mismatches 5; Indels 0; Gaps 0;	
QY	4 DIVMTQSPSSLSVSAAGEKVTMSCKSSQSLNSRNQKNYLAWYQKPGQPPKLLIYG 63	
DB	1 ELVMTQSPSSLSVSAAGEKVTMSCKSSQSLNSRNQKNYLAWYQKPGQPPKLLIYG 60	
QY	64 DSGVPDRFTGSGSGTDFLTITSSVQAEIDLAVYYCQNDHIYPYTFGGGKLEIK 116	
DB	61 ESGVPDRFTGSGSGTDFLTITSSVQAEIDLAVYYCQNDHSYPYTFGGGKLEIK 113	

RESULT 4	
ID	AD283525
XX	AD283525 standard; protein; 113 AA.
AC	AD283525;
XX	14-JUL-2005 (first entry)
DT	XX
DE	AntiEpCam single chain antibody SEQ ID NO 147.
XX	neoplasm; inflammation; immune disorder; infection; allergy;
KW	graft versus host disease; Cytostatic; Antiinflammatory;
KW	Immunosuppressive; Virucide; Antibacterial; Antiallergic; Antiparasitic;
KW	EpCam; antibody.
OS	Synthetic.
XX	WO2005040220-A1.
PN	06-MAY-2005.
XX	15-OCT-2004; 2004WO-EP011646.
PF	16-OCT-2003; 2003EP-00023581.
PR	(MICK-) MICROMET AG.
XX	Hofmeister R, Kohleisen B, Lenkner-Schuetz U, Itin C, Baeuerle P;
PI	Carr FJ, Hamilton AA, Williams S;
XX	WPI; 2005-333494/34.
DR	N-PSDB; AD283524.
XX	New cytotoxically active CD3 specific binding construct comprises a first
PT	domain specifically binding to human CD3 and an Ig-derived second binding
PT	domain, useful for treating, preventing, or ameliorating, e.g.
PT	proliferative disease.
XX	Example 8; SEQ ID NO 147; 639pp; English.
PS	The invention relates to a cytotoxically active CD3 specific binding
CC	construct comprising a first domain specifically binding to human CD3 and
CC	an Ig-derived second binding domain. The CD3 specific binding construct
CC	above or the construct produced by the process, nucleic acid molecule,
CC	vector, or host is useful for the preparation of a pharmaceutical
CC	composition for the prevention, treatment, or amelioration of a
CC	proliferative disease, a tumor, an inflammatory disease, an immunological
CC	disorder, an autoimmune disease, an infectious disease, viral disease,
CC	allergic reactions, parasitic reactions, graft-versus-host diseases, or
CC	host-versus-graft diseases. The cytotoxically active CD3 specific binding
CC	construct is useful for treating, preventing, or ameliorating
CC	proliferative disease, a tumor, an inflammatory disease, an immunological
CC	disorder, an autoimmune disease, an infectious disease, viral disease,
CC	allergic reactions, parasitic reactions, graft-versus-host diseases, or
CC	host-versus-graft diseases. The present sequence represents the amino
CC	acid sequence of an anti-EpCam single chain antibody.
XX	Sequence 113 AA;
SQ	
Query Match 89.9%; Score 545; DB 9; Length 113;	
Best Local Similarity 92.0%; Pred. No. 3.1e-38;	
Matches 104; Conservative 4; Mismatches 5; Indels 0; Gaps 0;	
QY	4 DIVMTQSPSSLSVSAGEKVTMSCKSSQSLNSRQKNYLAWYQKPGQPPKLLIYGAFTR 63
DB	1 ELVMTQSPSSLSVSAGEKVTMSCKSSQSLNSRQKNYLAWYQKPGQPPKLLIYGAFTR 60
QY	64 DSGVPRFTGSGSGDTFTLTISVQAEADVYCONDHIYPYTFGGGTKEIK 116
DB	61 ESGVPRFTGSGSGDTFTLTISVQAEADVYCONDHIYPYTFGGGTKEIK 113

RESULT 5	
ID	AAV17960
XX	AAV17960 standard; protein; 248 AA.
AC	AAV17960;
XX	04-AUG-1999 (first entry)
DT	XX
DE	Mouse scFV fragment 4-1.
XX	Binding site domain; BSD; epitope; fusion protein; therapeutic; cancer;
KW	autoimmune disease; scFv-antibody; single-chain Fv; mouse.
OS	Mus sp.
XX	WO9925818-A1.
PN	27-MAY-1999.
PD	16-NOV-1998; 98WO-EP007313.
PF	17-NOV-1997; 97EP-00120096.
PR	(KUPE/) KUPER P.
XX	Kufer P, Raum T, Borschert K, Zettl F, Lutterbues R;
PI	WPI; 1999-338004/28.
DR	N-PSDB; AAX77243.
XX	Phage display system for identification of binding site domains retaining
PT	capacity to bind an epitope.
PT	Claim 27; Fig 6.6; 152pp; English.
PS	The invention relates to a method of identifying binding site domains
XX	(BSD) that retain the capacity of binding to a predetermined epitope when
CC	positioned C-terminal of at least one further domain in a recombinant bi-
CC	or multivalent polypeptide. The method comprises (a) testing a panel of
CC	BSD displayed on the surface of a biological display system as part of a
CC	fusion protein for binding to a predetermined epitope, where the fusion
CC	protein comprises an additional domain positioned N-terminal of the BSD
CC	and an amino acid sequence that mediates anchoring of the fusion protein
CC	to the surface of the display system; and (b) identifying a BSD that
CC	binds to the predetermined epitope. The method is useful to identify bi-
CC	or multivalent polypeptides that comprise antibody binding sites capable
CC	of efficiently binding to the corresponding antigen. The polypeptides or
CC	antibodies identified by the method are useful therapeutically and
CC	diagnostically, for e.g. cancer and autoimmune diseases. scFv-antibody
CC	fragments that bind independently of their position within bifunctional
CC	single-chain fusion proteins can be isolated from combinatorial antibody
CC	libraries using the new in vitro method. Sequences AAV17957-965 represent
CC	mouse scFV fragments
XX	Sequence 248 AA;
SQ	
Query Match 89.9%; Score 545; DB 2; Length 248;	
Best Local Similarity 92.0%; Pred. No. 6.7e-38;	
Matches 104; Conservative 4; Mismatches 5; Indels 0; Gaps 0;	
QY	4 DIVMTQSPSSLSVSAGEKVTMSCKSSQSLNSRQKNYLAWYQKPGQPPKLLIYGAFTR 63
DB	136 ELVMTQSPSSLSVSAGEKVTMSCKSSQSLNSRQKNYLAWYQKPGQPPKLLIYGAFTR 195
QY	64 DSGVPRFTGSGSGDTFTLTISVQAEADVYCONDHIYPYTFGGGTKEIK 116
DB	196 ESGVPRFTGSGSGDTFTLTISVQAEADVYCONDHIYPYTFGGGTKEIK 248

RESULT 6	
ID	AD283445
XX	AD283445 standard; protein; 497 AA.

AC ADZ83445;
XX
DT 14-JUL-2005 (first entry)
XX
DE CD3 specific binding construct SEQ ID NO 67.
XX
DE neoplasm; inflammation; immune disorder; infection; allergy;
KW graft versus host disease; Cytostatic; Antiinflammatory;
KW Immunosuppressive; Virucide; Antibacterial; Antiallergic; Antiparasitic.
XX
OS Synthetic.
XX
XX WO2005040220-A1.
XX
XX PD 06-MAY-2005.
XX
XX PF 15-OCT-2004; 2004WO-EP011646.
XX
XX PR 16-OCT-2003; 2003EP-00023581.
XX
XX PA (MICR-) MICROMET AG.
XX
XX PI Hofmeister R, Kohleisen B, Lenkkeri-Schuetz U, Itin C, Baeuerle P;
PI Carr FJ, Hamilton AA, Williams S;
XX
XX DR N-PSDB; ADZ83444.
XX
XX DR N-PSDB; ADZ83444.
XX
XX PT New cytotoxicity active CD3 specific binding construct comprises a first
PT domain specifically binding to human CD3 and an Ig-derived second binding
PT domain, useful for treating, preventing, or ameliorating, e.g.
PT proliferative disease.
XX
XX PS Claim 20; SEQ ID NO 67; 639pp; English.
XX
XX CC The invention relates to a cytotoxicity active CD3 specific binding
CC construct comprising a first domain specifically binding to human CD3 and
CC an Ig-derived second binding domain. The CD3 specific binding construct
CC above or the construct produced by the process, nucleic acid molecule,
CC vector, or host is useful for the preparation of a pharmaceutical
CC composition for the prevention, treatment, or amelioration of a
CC proliferative disease, a tumor, an inflammatory disease, an immunological
CC disorder, an autoimmune disease, an infectious disease, viral disease,
CC allergic reactions, parasitic reactions, graft-versus-host diseases, or
CC host-versus-graft diseases. The cytotoxicity active CD3 specific binding
CC construct is useful for treating, preventing, or ameliorating
CC proliferative disease, a tumor, an inflammatory disease, an immunological
CC disorder, an autoimmune disease, an infectious disease, viral disease,
CC allergic reactions, parasitic reactions, graft-versus-host diseases, or
CC host-versus-graft diseases. The present sequence represents the amino
CC acid sequence of a CD3 specific binding construct.
XX
SQ Sequence 497 AA;
Query Match 89.9%; Score 545; DB 9; Length 497;
Best Local Similarity 92.0%; Pred. No. 1.3e-37;
Matches 104; Conservative 4; Mismatches 5; Indels 0; Gaps 0;
QY 4 DIVMTQSPSSLSVSAAGEKVTMSCKSSQSLNSRNQKNYLAWYQKPGQPPKLLIYGVFIR 63
Db :::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::
385 ELVMTQSPSSLSVSAAGEKVTMSCKSSQSLNSRNQKNYLAWYQKPGQPPKLLIYGASTR 444
QY 64 DSGVPDRFTGSGSGTDFTLTISSVQAEADLAVYYCNDHIYPYTFGGGKLEIK 116
Db :::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::
445 ESGVPDRFTGSGSGTDFTLTISSVQAEADLAVYYCNDIYSPYTFGGGKLEIK 497
RESULT 7
ADV66137
ID ADV66137 standard; protein; 500 AA.
XX
XX AC ADV66137;
XX

DT 24-FEB-2005 (first entry)
XX
DE Anti-CD3-anti-EpCAM bispecific single chain antibody - SEQ ID 60.
XX
KW bispecific single chain antibody; epithelial cell adhesion molecule;
KW EpCAM; CD3; tumor; cancer; cytostatic.
XX
OS Unidentified.
XX
XX WO2004106383-A1.
XX
XX PD 09-DEC-2004.
XX
XX PF 26-MAY-2004; 2004WO-EP005687.
XX
XX PR 31-MAY-2003; 2003EP-00012133.
XX
XX PR 31-MAY-2003; 2003EP-00012134.
XX
XX PA (MICR-) MICROMET AG.
XX
XX PI Kufer P, Berry M, Offner S, Brischwein K, Wolf A, Raum T;
PI Kohleisen B, Lenkkeri-Schuetz U, Baeuerle P;
XX
XX DR WPI; 2005-021271/02.
XX
XX DR N-PSDB; ADV66136.
XX
XX PT New pharmaceutical composition having a bispecific single chain antibody
PT construct, useful for preventing, treating or ameliorating a tumorous
PT disease, such as an epithelial or minimal residual cancer.
XX
XX PS Claim 12; SEQ ID NO 60; 227pp; English.
XX
XX CC The invention comprises a composition that contains a bispecific single
CC chain antibody consisting of at least two domains, where one of domains
CC binds to human epithelial cell adhesion molecule (EpCAM) antigen, and the
CC second domain binds to human CD3 antigen. The bispecific antibody
CC construct of the invention is useful for the prevention, treatment or
CC amelioration of a tumorous disease, such as an epithelial or minimal
CC residual cancer. The present amino acid sequence represents a bispecific
CC single chain antibody of the invention.
XX
SQ Sequence 500 AA;
Query Match 89.9%; Score 545; DB 9; Length 500;
Best Local Similarity 92.0%; Pred. No. 1.4e-37;
Matches 104; Conservative 4; Mismatches 5; Indels 0; Gaps 0;
QY 4 DIVMTQSPSSLSVSAAGEKVTMSCKSSQSLNSRNQKNYLAWYQKPGQPPKLLIYGVFIR 63
Db :::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::
382 ELVMTQSPSSLSVSAAGEKVTMSCKSSQSLNSRNQKNYLAWYQKPGQPPKLLIYGASTR 441
QY 64 DSGVPDRFTGSGSGTDFTLTISSVQAEADLAVYYCNDHIYPYTFGGGKLEIK 116
Db :::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::
442 ESGVPDRFTGSGSGTDFTLTISSVQAEADLAVYYCNDIYSPYTFGGGKLEIK 494
RESULT 8
ADV66133
ID ADV66133 standard; protein; 503 AA.
XX
XX AC ADV66133;
XX
XX DT 24-FEB-2005 (first entry)
XX
XX DE Anti-CD3-anti-EpCAM bispecific single chain antibody - SEQ ID 56.
XX
KW bispecific single chain antibody; epithelial cell adhesion molecule;
KW EpCAM; CD3; tumor; cancer; cytostatic.
XX
OS Unidentified.
XX
XX WO2004106383-A1.
XX

PD 09-DEC-2004.
XX
PF 26-MAY-2004; 2004WO-EP005687.
XX
PR 31-MAY-2003; 2003EP-00012133.
PR 31-MAY-2003; 2003EP-00012134.
XX
PA (MICR-) MICROMET AG.
XX
PI Kufer P, Berry M, Offner S, Brischwein K, Wolf A, Raum T;
PI Kohleisen B, Lenkkeri-Schuetz U, Baeuerle P;
XX
DR WPI; 2005-021271/02.
DR N-PSDB; ADV66132.
XX
XX New pharmaceutical composition having a bispecific single chain antibody
PT construct, useful for preventing, treating or ameliorating a tumorous
PT disease, such as an epithelial or minimal residual cancer.
XX
PS Claim 12; SEQ ID NO 56; 227pp; English.
XX
CC The invention comprises a composition that contains a bispecific single
CC chain antibody consisting of at least two domains, where one of domains
CC binds to human epithelial cell adhesion molecule (EPCAM) antigen, and the
CC second domain binds to human CD3 antigen. The bispecific antibody
CC construct of the invention is useful for the prevention, treatment or
CC amelioration of a tumorous disease, such as an epithelial or minimal
CC residual cancer. The present amino acid sequence represents a bispecific
CC single chain antibody of the invention.
XX
SQ Sequence 503 AA;
XX
Query Match 89.9%; Score 545; DB 9; Length 503;
Best Local Similarity 92.0%; Pred. No. 1.4e-37;
Matches 104; Conservative 4; Mismatches 5; Indels 0; Gaps 0;
QY 4 DIVMTQSPSSLSVAGEKVTMSCKSSQSLNSRNQKNYLAWYQOKPGPPKLLIYGVFIR 63
DB 385 ELVMTQSPSSLSVAGEKVTMSCKSSQSLNSGNQKNYLAWYQOKPGPPKLLIYGASTR 444
QY 64 DSGVPRFTGSGSGTDFTLTISSVQAEADLAVYVCQNDHIYPYTFGGGTTKLEIK 116
DB 445 ESGVPRFTGSGSGTDFTLTISSVQAEADLAVYVCQNDIYPYTFGGGTTKLEIK 497
XX
RESULT 9
ADV66135
ID ADV66135 standard; protein; 503 AA.
XX
AC ADV66135;
XX
DT 24-FEB-2005 (first entry)
XX
DE Anti-CD3-anti-EPCAM bispecific single chain antibody - SEQ ID 58.
XX
KW bispecific single chain antibody; epithelial cell adhesion molecule;
KW EPCAM; CD3; tumor; cancer; cytostatic.
XX
OS Unidentified.
XX
PN WO2004106383-A1.
XX
PD 09-DEC-2004.
XX
PF 26-MAY-2004; 2004WO-EP005687.
XX
PR 31-MAY-2003; 2003EP-00012133.
PR 31-MAY-2003; 2003EP-00012134.
XX
PA (MICR-) MICROMET AG.
XX
PI Kufer P, Berry M, Offner S, Brischwein K, Wolf A, Raum T;
PI Kohleisen B, Lenkkeri-Schuetz U, Baeuerle P;

XX WPI; 2005-021271/02.
DR N-PSDB; ADV66134.
XX
PT New pharmaceutical composition having a bispecific single chain antibody
PT construct, useful for preventing, treating or ameliorating a tumorous
PT disease, such as an epithelial or minimal residual cancer.
XX
PS Claim 12; SEQ ID NO 58; 227pp; English.
XX
CC The invention comprises a composition that contains a bispecific single
CC chain antibody consisting of at least two domains, where one of domains
CC binds to human epithelial cell adhesion molecule (EPCAM) antigen, and the
CC second domain binds to human CD3 antigen. The bispecific antibody
CC construct of the invention is useful for the prevention, treatment or
CC amelioration of a tumorous disease, such as an epithelial or minimal
CC residual cancer. The present amino acid sequence represents a bispecific
CC single chain antibody of the invention.
XX
SQ Sequence 503 AA;
XX
Query Match 89.9%; Score 545; DB 9; Length 503;
Best Local Similarity 92.0%; Pred. No. 1.4e-37;
Matches 104; Conservative 4; Mismatches 5; Indels 0; Gaps 0;
QY 4 DIVMTQSPSSLSVAGEKVTMSCKSSQSLNSRNQKNYLAWYQOKPGPPKLLIYGVFIR 63
DB 385 ELVMTQSPSSLSVAGEKVTMSCKSSQSLNSGNQKNYLAWYQOKPGPPKLLIYGASTR 444
QY 64 DSGVPRFTGSGSGTDFTLTISSVQAEADLAVYVCQNDHIYPYTFGGGTTKLEIK 116
DB 445 ESGVPRFTGSGSGTDFTLTISSVQAEADLAVYVCQNDIYPYTFGGGTTKLEIK 497
XX
RESULT 10
ADZ83436
ID ADZ83436 standard; protein; 515 AA.
XX
AC ADZ83436;
XX
DT 14-JUL-2005 (first entry)
XX
DE Deimmunized construct 4-1xanti-CD3.
XX
KW neoplasm; inflammation; immune disorder; infection; allergy;
KW graft versus host disease; Cytostatic; Antiinflammatory;
KW Immunosuppressive; Virucide; Antibacterial; Antiallergic; Antiparasitic.
XX
OS Synthetic.
XX
PN WO2005040220-A1.
XX
PD 06-MAY-2005.
XX
PF 15-OCT-2004; 2004WO-EP011646.
XX
PR 16-OCT-2003; 2003EP-00023581.
XX
PA (MICR-) MICROMET AG.
XX
PI Hofmeister R, Kohleisen B, Lenkkeri-Schuetz U, Itin C, Baeuerle P;
PI Carr FU, Hamilton AA, Williams S;
XX
DR WPI; 2005-333494/34.
DR N-PSDB; ADZ83435.
XX
XX New cytotoxically active CD3 specific binding construct comprises a first
PT domain specifically binding to human CD3 and an Ig-derived second binding
PT domain, useful for treating, preventing, or ameliorating, e.g.
PT proliferative disease.
XX
PS Claim 20; SEQ ID NO 58; 639pp; English.
XX

CC The invention relates to a cytotoxically active CD3 specific binding
CC construct comprising a first domain specifically binding to human CD3 and
CC an Ig-derived second binding domain. The CD3 specific binding construct
CC above or the construct produced by the process, nucleic acid molecule,
CC vector, or host is useful for the preparation of a pharmaceutical
CC composition for the prevention, treatment, or amelioration of a
CC proliferative disease, a tumor, an inflammatory disease, an immunological
CC disorder, an autoimmune disease, an infectious disease, viral disease,
CC allergic reactions, parasitic reactions, graft-versus-host diseases, or
CC host-versus-graft diseases. The cytotoxically active CD3 specific binding
CC construct is useful for treating, preventing, or ameliorating
CC proliferative disease, a tumor, an inflammatory disease, an immunological
CC disorder, an autoimmune disease, an infectious disease, viral disease,
CC allergic reactions, parasitic reactions, graft-versus-host diseases, or
CC host-versus-graft diseases. The present sequence represents the amino
CC acid sequence of delimmunized construct 4-ixanti-CD3.

XX Sequence 515 AA;

Query Match 89.9%; Score 545; DB 9; Length 515;
Best Local Similarity 92.0%; Pred. No. 1.4e-37;
Matches 104; Conservative 4; Mismatches 5; Indels 0; Gaps 0;

QY 4 DIVMTQSPSSLSVSAAGEKVTMSCKSSQSLNRSNOKNYLAWYQKPGQPPKLLIYGVFIR 63
XX :|||||
DB 20 ELVMTQSPSSLSVSAAGEKVTMSCKSSQSLNRSNOKNYLAWYQKPGQPPKLLIYGASTR 79
XX :|||||

QY 64 DSGVPDRFTGSGSGTDFLTITSSVQAEGLAVYYCONDHIYPYTFGGGKLEIK 116
XX :|||||
DB 80 ESGVPDRFTGSGSGTDFLTITSSVQAEGLAVYYCONDYSYPYTFGGGKLEIK 132
XX :|||||

RESULT 11

ADV66116
ID ADV66116 standard; protein; 521 AA.

XX ADV66116;

XX 24-FEB-2005 (first entry)

DE Anti-CD3-anti-EpCAM bispecific single chain antibody - SEQ ID 39.

XX bispecific single chain antibody; epithelial cell adhesion molecule;
KW EpCAM; CD3; tumor; cancer; cytostatic.

XX Unidentified.

XX WO2004106383-A1.

XX 09-DEC-2004.

PF 26-MAY-2004; 2004WO-EP005687.

XX 31-MAY-2003; 2003EP-00012133.

PR 31-MAY-2003; 2003EP-00012134.

XX (MICR-) MICROMET AG.

XX Kufer P, Berry M, Offner S, Brieschwein K, Wolf A, Raum T;

PI Kohleisen B, Lenkner-Schuetz U, Baeuerle P;

XX WPI; 2005-021271/02.

DR N-PSDB; ADV66115.

XX New pharmaceutical composition having a bispecific single chain antibody
PT construct, useful for preventing, treating or ameliorating a tumorous
PT disease, such as an epithelial or minimal residual cancer.

XX Claim 12; SEQ ID NO 39; 227pp; English.

XX The invention comprises a composition that contains a bispecific single
CC chain antibody consisting of at least two domains, where one of domains
CC binds to human epithelial cell adhesion molecule (EpCAM) antigen, and the

CC second domain binds to human CD3 antigen. The bispecific antibody
CC construct of the invention is useful for the prevention, treatment or
CC amelioration of a tumorous disease, such as an epithelial or minimal
CC residual cancer. The present amino acid sequence represents a bispecific
CC single chain antibody of the invention.

XX Sequence 521 AA;

Query Match 89.9%; Score 545; DB 9; Length 521;
Best Local Similarity 92.0%; Pred. No. 1.4e-37;
Matches 104; Conservative 4; Mismatches 5; Indels 0; Gaps 0;

QY 4 DIVMTQSPSSLSVSAAGEKVTMSCKSSQSLNRSNOKNYLAWYQKPGQPPKLLIYGVFIR 63
XX :|||||

DB 20 ELVMTQSPSSLSVSAAGEKVTMSCKSSQSLNRSNOKNYLAWYQKPGQPPKLLIYGASTR 79
XX :|||||

QY 64 DSGVPDRFTGSGSGTDFLTITSSVQAEGLAVYYCONDHIYPYTFGGGKLEIK 116
XX :|||||

DB 80 ESGVPDRFTGSGSGTDFLTITSSVQAEGLAVYYCONDYSYPYTFGGGKLEIK 132
XX :|||||

RESULT 12

AAB62864

ID AAB62864 standard; protein; 114 AA.

XX AAB62864;

XX 15-MAY-2001 (first entry)

DE Anti-SAF-1 monoclonal antibody 13G3 kappa chain variable region protein.

XX Sialoadhesin factor-1; SAF-1; anti-SAF-1 monoclonal antibody; 13G3; 11G4;

KW osteomyelitis; wound infection; sepsis; Listeria monocytogene;

KW Salmonella; Leishmania; kappa chain variable region; mouse.

XX Mus musculus.

XX WO200112646-A1.

XX 22-FEB-2001.

XX 18-AUG-2000; 2000WO-US022663.

XX 19-AUG-1999; 99US-0149753P.

XX (SMIK) SMITHKLINE BEECHAM CORP.

PA (SMIK) SMITHKLINE BEECHAM PLC.

XX Erickson-Miller CL, Holmes SD, King AG, Taylor AH;

XX WPI; 2001-211197/21.

DR N-PSDB; AAF62143.

XX New sialoadhesin factor-1 agonist antibody having the characteristic of
PT monoclonal antibody 13G3 or 11G4 for treating osteomyelitis, deep seated
PT wound infections and antibiotic resistant bacterial infections.

XX Claim 19; Fig 2; 43pp; English.

XX This invention relates to sialoadhesin factor-1 (SAF-1) monoclonal
CC antibodies 13G3 and 11G4. A neutrophil-priming dose of SAF-1 agonist
CC antibody or a pharmaceutical composition comprising the antibody is
CC useful for treating or preventing an infectious disease state such as
CC osteomyelitis, deep seated wound infections, sepsis, antibiotic resistant
CC bacterial infection, viral infections and those involving intracellular
CC pathogens and parasites such as Listeria monocytogenes, Salmonella and
CC Leishmania in a mammal. Nucleic acid sequences encoding the variable
CC light chain and heavy chain peptide sequences are useful for mutagenic
CC introduction of specific changes within the nucleic acid sequences
CC encoding the (complementarity determining regions) CDRs or framework
CC regions, and for incorporation of the resulting modified or fusion
CC nucleic acid sequence into a plasmid for expression. The CDR-encoding
CC regions comprising silent mutations are used in construction of humanized

CC antibodies or other engineered antibodies. The present sequence
CC represents anti-SAF-1 monoclonal antibody 13G3 kappa chain variable
CC region amino acid sequence
SQ Sequence 114 AA;
Query Match 89.1%; Score 540; DB 4; Length 114;
Best Local Similarity 91.2%; Pred. No. 8.2e-38;
Matches 103; Conservative 4; Mismatches 6; Indels 0; Gaps 0;
QY 4 DIVMTQSPSSLSVAGEKVTMSCKSSQSLNSRNQKNYLAWYQOKPGQPPKLLIYGVFIR 63
Db 1 DIVMTQSPSSLSVAGEKVTMSCKSSQSLNSRNQKNYLAWYQOKPGQPPKLLIYGASTR 60
QY 64 DSGVPRFTGSGSGTDTFTLTISVQAEEDLAVYYQNDHIYPYTFGGGSKLEIK 116
Db 61 ESVGPRFTGSGSGTDTFTLTISVQAEEDLAVYYQNEHSYPTFGSGTKLEIK 113
RESULT 13
AAR38603
ID AAR38603 standard; protein; 113 AA.
XX AAR38603;
XX 25-MAR-2003 (revised)
DT 28-OCT-1993 (first entry)
XX MCPC light chain.
XX Antibody; variable domain; light; L; heavy; H; consensus; affinity;
KW antigen; immunogenicity; humanisation; framework.
XX Homo sapiens.
XX Key Location/Qualifiers
FH Misc-difference 31..36
FT /note= "variation in length of hypervariable loop
FT sequences among antibodies"
XX
XX WO9311794-A1.
XX 24-JUN-1993.
XX 14-DEC-1992; 92WO-US010906.
XX 13-DEC-1991; 91US-00808464.
XX (XOMA) XOMA CORP.
XX Studnicka GM, Little RG, Fishwild DM, Kohn FR;
XX WPI; 1993-213827/26.
XX Antibodies prepn. used for treatment of auto-immune diseases - by
PT replacement of critical residues to reduce immunogenicity but retain
PT binding affinity, etc.
XX Disclosure; Page 85; 160pp; English.
XX The amino acid sequences of the light and heavy chains of the variable
CC domains from antibodies HVH [HYHEL-10 Fab-lysozyme complex] (AAR38601 and
CC AAR38608, respectively), MCPC [IGA Fab MCP603-phosphocholine complex]
CC (AAR38602-03 and AAR38609-10, respectively), NEWM [Ig Fab' NEW] (AAR38604
CC -05 and AAR38611, respectively) and KOL [IgG1 KOL] (AAR38606-07 and
CC AAR38612, respectively) may be used to determine an alignment from which
CC appropriate changes may be made. Unlike other methods of humanisation,
CC which advocate the replacement of entire antibody framework regions with
CC those of human antibodies, this method involves only the introduction of
CC human residues into those positions not critical for antigen binding.
CC This ensures that the binding properties of the modified antibody are not
CC diminished. (Updated on 25-MAR-2003 to correct PN field.)
XX

SQ Sequence 113 AA;
Query Match 88.4%; Score 536; DB 2; Length 113;
Best Local Similarity 91.2%; Pred. No. 1.8e-37;
Matches 103; Conservative 3; Mismatches 7; Indels 0; Gaps 0;
QY 4 DIVMTQSPSSLSVAGEKVTMSCKSSQSLNSRNQKNYLAWYQOKPGQPPKLLIYGVFIR 63
Db 1 DIVMTQSPSSLSVAGEKVTMSCKSSQSLNSRNQKNYLAWYQOKPGQPPKLLIYGASTR 60
QY 64 DSGVPRFTGSGSGTDTFTLTISVQAEEDLAVYYQNDHIYPYTFGGGSKLEIK 116
Db 61 ESVGPRFTGSGSGTDTFTLTISVQAEEDLAVYYQNDHSYPTFGAGTKLEIK 113
RESULT 14
AAR68742
ID AAR68742 standard; protein; 113 AA.
XX AAR68742;
XX AC
XX 25-MAR-2003 (revised)
DT 15-JUL-1995 (first entry)
XX MAb MCP603 light chain.
XX Monoclonal antibody; MCP603; disulfide bond; heavy chain; light chain;
KW variable region; Fv; antibody engineering; ligand binding moiety;
KW immunotoxin.
XX Mus sp.
XX Key Location/Qualifiers
FH Region 1..23
FT /label= PR1
FT /note= "framework region 1"
FT Region 24..40
FT /label= CDR1
FT /note= "complementarity determining region 1"
FT Region 41..55
FT /label= PR2
FT /note= "framework region 2"
FT Modified-site 49
FT /note= "residue at position 49 can be changed to Cys for
FT possible interchain disulfide bond"
FT Region 56..62
FT /label= CDR2
FT /note= "complementarity determining region 2"
FT Region 63..94
FT /label= PR3
FT /note= "framework region 3"
FT Region 95..103
FT /label= CDR3
FT /note= "complementarity determining region 3"
FT Modified-site 97
FT /note= "Ser to Tyr mutation site"
FT Region 104..113
FT /label= PR4
FT /note= "framework region 4"
FT Modified-site 106
FT /note= "residue at position 106 can be changed to Cys for
FT possible interchain disulfide bond"
XX WO9429350-A2.
XX 22-DEC-1994.
XX 14-JUN-1994; 94WO-US005687.
XX 14-JUN-1993; 93US-00077252.
XX (USSH) US DEPT HEALTH & HUMAN SERVICES.
XX

PI Pastan IH, Lee B, Jung S, Brinkmann U;
DR WPI; 1995-036408/05.
XX New ligand-binding polypeptide(s) - having a disulphide bond linking
PT framework regions of first and second variable regions of ligand binding
PT moieties.
XX
PS Disclosure; Page 53; 67pp; English.
XX The polypeptide given in AAW58472 corresponds to the light chain of MAB
CC McPC603. This MAB was used to generate a model of MAB B3(Fv), which has
CC been used in the construction of disulfide bond-stabilized Fv fragments
CC used as immunotoxins. (Updated on 25-MAR-2003 to correct PN field.)
XX
SQ Sequence 113 AA;
Query Match 88.4%; Score 536; DB 2; Length 113;
Best Local Similarity 91.2%; Pred. No. 1.8e-37;
Matches 103; Conservative 3; Mismatches 7; Indels 0; Gaps 0;
QY 4 DIVMTQSPSSLSVSAGEKVTMSCKSSQSLNSRNQKNYLAWYQKPGQPPKLLIYGVFIR 63
Db 1 DIVMTQSPSSLSVSAGEKVTMSCKSSQSLNSGNQKNFLAWYQKPGQPPKLLIYGASTR 60
QY 64 DSGVPDRFTGSGSGTDFLTITSSVQAE DLAVYYQNDHIYPVTFGGGKLEIK 116
Db 61 ESGVPDRFTGSGSGTDFLTITSSVQAE DLAVYYQNDHSYPLTFGAGTKLEIK 113
Search completed: May 19, 2006, 17:40:05
Job time : 138.333 secs

RESULT 15
AAW58483
ID AAW58483 standard; protein; 113 AA.
XX
AC AAW58483;
XX
DT 18-AUG-1998 (first entry)
XX
DE Murine MCPC antibody light chain variable domain.
XX
KW Humanised; human; mouse; CD5; anti-CD5 antibody; immunoglobulin;
KW depletion; cytotoxic; immunoconjugate; fusion protein; psoriasis;
KW autoimmune disease; rheumatoid arthritis; type I diabetes.
OS Mus sp.
XX
PN US5770196-A.
XX
PD 23-JUN-1998.
XX
PF 07-JUN-1995; 95US-00472788.
XX
PR 13-DEC-1991; 91US-00808464.
PR 14-DEC-1992; 92WO-US010906.
PR 23-JUN-1993; 93US-00082842.
XX
PA (XOMA) XOMA CORP.
XX
PI Studnicka GM;
XX
DR WPI; 1998-376744/32.
XX
PT Depletion of CD5-positive cells in vivo - using anti-CD5 antibodies with
PT humanised variable regions.
XX
PS Disclosure; Col 43-44; 77pp; English.
XX
CC A method has been developed of depleting CD5+ cells in an animal. The
CC method comprises administering a cytotoxic protein containing a modified
CC immunoglobulin (Ig) variable domain, where the protein is an anti-CD5 Ig
CC molecule or an immunoconjugate or fusion protein containing an anti-CD5
CC Ig molecule, and where the modified Ig variable domain comprises at least
CC one of (a) a modified light chain variable region (see AAW58478 or

Query Match 88.4%; Score 536; DB 2; Length 112;
Best Local Similarity 92.0%; Pred. No. 2.4e-40;
Matches 103; Conservative 2; Mismatches 7; Indels 0; Gaps 0;

QY 4 DIVMTQSPSSLSVSGAGEKVTMTSCSSQSLLNSRNQKNYLAWYQKPGPPKLLIYGVFIR 63
DB 1 DIVMTQSPSSLSVSGAGEKVTMTSCSSQSLLNSRNQKNYLAWYQKPGPPKLLIYGASTR 60

QY 64 DSGVPDRFTGSGSGTDFLTITSSVQAEADLAVYYCNDHIYPYTFGGGKLEI 115
DB 61 ESGVPDRFTGSGSGTDFLTITSSVQAEADLAVYYCNDHSYPLTFGAGTKLEL 112

RESULT 3
E30538
Ig kappa chain V region (253.12D3) - mouse (fragment)
C:Species: Mus musculus (house mouse)
C:Date: 10-Feb-1989 #sequence_revision 10-Feb-1989 #text_change 21-Jan-2000
C:Accession: E30538
R:Clafalin, J.L.; Berry, J.
J. Immunol. 141, 4012-4019, 1988
A:Title: Genetics of the phosphocholine-specific antibody response to Streptococcus pneumoniae
A:Reference number: A30534; MUID:89035545; PMID:3141511
A:Accession: E30538
A:Status: preliminary; nucleic acid sequence not shown; not compared with conceptual translation
A:Molecule type: mRNA
A:Residues: 1-112 <CLA>
A:CROSS-references: UNIPARC:UPI0000176CD4
C:Superfamily: immunoglobulin V region; immunoglobulin homology
C:Keywords: heterotetramer; immunoglobulin
F:16-96/Domain: immunoglobulin homology <IMM>

Query Match 88.4%; Score 536; DB 2; Length 112;
Best Local Similarity 92.0%; Pred. No. 2.4e-40;
Matches 103; Conservative 2; Mismatches 7; Indels 0; Gaps 0;

QY 4 DIVMTQSPSSLSVSGAGEKVTMTSCSSQSLLNSRNQKNYLAWYQKPGPPKLLIYGVFIR 63
DB 1 DIVMTQSPSSLSVSGAGEKVTMTSCSSQSLLNSRNQKNYLAWYQKPGPPKLLIYGASTR 60

QY 64 DSGVPDRFTGSGSGTDFLTITSSVQAEADLAVYYCNDHIYPYTFGGGKLEI 115
DB 61 ESGVPDRFTGSGSGTDFLTITSSVQAEADLAVYYCNDHSYPLTFGAGTKLEL 112

RESULT 4
P10264
Ig kappa chain V region (anti-DNA, D20VK) - mouse (fragment)
C:Species: Mus musculus (house mouse)
C:Date: 16-Sep-1992 #sequence_revision 16-Sep-1992 #text_change 21-Jan-2000
R:Shlomchik, M.; Mascelll, M.; Shan, H.; Radic, M.Z.; Pisetsky, D.; Marshak-Rothstein, A.
J. Exp. Med. 171, 265-297, 1990
A:Title: Anti-DNA antibodies from autoimmune mice arise by clonal expansion and somatic hypermutation
A:Reference number: P10231; MUID:90111618; PMID:2104919
A:Accession: P10264
A:Molecule type: mRNA
A:Residues: 1-113 <SHL>
A:CROSS-references: UNIPARC:UPI0000176AFB
C:Superfamily: immunoglobulin V region; immunoglobulin homology
C:Keywords: heterotetramer; immunoglobulin
F:1-23/Region: framework 1
F:16-96/Domain: immunoglobulin homology <IMM>
F:24-40/Region: complementarity-determining 1
F:41-55/Region: framework 2
F:56-62/Region: complementarity-determining 2
F:63-94/Region: framework 3
F:95-103/Region: complementarity-determining 3
F:104-113/Region: framework 4

Query Match 87.6%; Score 531; DB 2; Length 113;
Best Local Similarity 90.3%; Pred. No. 6.8e-40;
Matches 102; Conservative 4; Mismatches 7; Indels 0; Gaps 0;

QY 4 DIVMTQSPSSLSVSGAGEKVTMTSCSSQSLLNSRNQKNYLAWYQKPGPPKLLIYGVFIR 63
DB 1 DIVMTQSPSSLSVSGAGEKVTMTSCSSQSLLNSRNQKNYLAWYQKPGPPKLLIYGASTR 60

QY 64 DSGVPDRFTGSGSGTDFLTITSSVQAEADLAVYYCNDHIYPYTFGGGKLEI 116
DB 61 ESGVPDRFTGSGSGTDFLTITSSVQAEADLAVYYCNDYSYPLTFGAGTKLEL 113

RESULT 5
E30535
Ig kappa chain V region (6D10) - mouse (fragment)
C:Species: Mus musculus (house mouse)
C:Date: 23-Feb-1989 #sequence_revision 23-Feb-1989 #text_change 21-Jan-2000
C:Accession: E30535
R:Clafalin, J.L.; Berry, J.; Flaherty, D.; Dunnick, W.
J. Immunol. 138, 3060-3068, 1987
A:Title: Somatic evolution of diversity among anti-phosphocholine antibodies induced with J. Immunol. 138, 3060-3068, 1987
A:Reference number: A30556; MUID:87196439; PMID:3106498
A:Accession: E30535
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-108 <CLA>
A:CROSS-references: UNIPARC:UPI0000176AED
A:Note: the sequence was determined from the differentiated gene
C:Superfamily: immunoglobulin V region; immunoglobulin homology
C:Keywords: heterotetramer; immunoglobulin
F:16-96/Domain: immunoglobulin homology <IMM>

Query Match 85.8%; Score 520; DB 2; Length 108;
Best Local Similarity 92.6%; Pred. No. 6e-39;
Matches 100; Conservative 1; Mismatches 7; Indels 0; Gaps 0;

QY 4 DIVMTQSPSSLSVSGAGEKVTMTSCSSQSLLNSRNQKNYLAWYQKPGPPKLLIYGVFIR 63
DB 1 DIVMTQSPSSLSVSGAGEKVTMTSCSSQSLLNSRNQKNYLAWYQKPGPPKLLIYGASTR 60

QY 64 DSGVPDRFTGSGSGTDFLTITSSVQAEADLAVYYCNDHIYPYTFGGGT 111
DB 61 ESGVPDRFTGSGSGTDFLTITSSVQAEADLAVYYCNDHSYPLTFGAGT 108

RESULT 6
G30535
Ig kappa chain V region (2G6) - mouse (fragment)
C:Species: Mus musculus (house mouse)
C:Date: 23-Feb-1989 #sequence_revision 23-Feb-1989 #text_change 21-Jan-2000
C:Accession: G30535
R:Clafalin, J.L.; Berry, J.; Flaherty, D.; Dunnick, W.
J. Immunol. 138, 3060-3068, 1987
A:Title: Somatic evolution of diversity among anti-phosphocholine antibodies induced with J. Immunol. 138, 3060-3068, 1987
A:Reference number: A30556; MUID:87196439; PMID:3106498
A:Accession: G30535
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-107 <CLA>
A:CROSS-references: UNIPARC:UPI0000176AF6
A:Note: the sequence was determined from the differentiated gene
C:Superfamily: immunoglobulin V region; immunoglobulin homology
C:Keywords: heterotetramer; immunoglobulin
F:16-96/Domain: immunoglobulin homology <IMM>

Query Match 85.0%; Score 515; DB 2; Length 107;
Best Local Similarity 92.5%; Pred. No. 1.6e-38;
Matches 99; Conservative 1; Mismatches 7; Indels 0; Gaps 0;

QY 4 DIVMTQSPSSLSVSGAGEKVTMTSCSSQSLLNSRNQKNYLAWYQKPGPPKLLIYGVFIR 63
DB 1 DIVMTQSPSSLSVSGAGEKVTMTSCSSQSLLNSRNQKNYLAWYQKPGPPKLLIYGASTR 60

QY 64 DSGVPDRFTGSGSGTDFLTITSSVQAEADLAVYYCNDHIYPYTFGGG 110

Db 61 ESGVPRFTGSGSGTDTLTITSSVQAEADLAVVYQNDHSYPLTFGAG 107

RESULT 7
F30535
Ig kappa chain V region (5G4) - mouse (fragment)
C:Species: Mus musculus (house mouse)
C:Date: 23-Feb-1989 #sequence_revision 23-Feb-1989 #text_change 21-Jan-2000
C:Accession: F30535
R;Claflin, J.L.; Berry, J.; Flaherty, D.; Dunnick, W.
J. Immunol. 138, 3060-3068, 1987
A:Title: Somatic evolution of diversity among anti-phosphocholine antibodies induced with J. Immunol. 138, 3060-3068, 1987
A:Reference number: A30556; MUID:87196439; PMID:3106498
A:Accession: F30535
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-107 <CLA>
A:Cross-references: UNIPARC:UPI0000176AF5
A:Note: the sequence was determined from the differentiated gene
C:Superfamily: immunoglobulin V region; immunoglobulin homology
C:Keywords: heterotrimer; immunoglobulin
F;16-96/Domain: immunoglobulin homology <IMM>

Query Match 84.5%; Score 512; DB 2; Length 107;
Best Local Similarity 91.8%; Pred. No. 3e-38;
Matches 98; Conservative 2; Mismatches 7; Indels 0; Gaps 0;

QY 4 DIVMTQSPSSLSVAGEKVTMSCKSSQSLNSGNQKNYLAWYQKPGQPPKLLIYGVFIR 63
DB 1 DIVMTQSPSSLSVAGEKVTMSCKSSQSLNSGNQKNYLAWYQKPGQPPKLLIYGASTR 60

QY 64 DSGVPRFTGSGSGTDTLTITSSVQAEADLAVVYQNDHIIYPYTFGGG 110
DB 61 ESGVPRFTGSGSGTDTLTITSSVQAEADLAVVYQNDHSYPLTFGAG 107

RESULT 8
PL0263
Ig kappa chain V region (anti-DNA, S57VK, S41VK, S54VK, S7VK and S204VK) - mouse (fragment)
C:Species: Mus musculus (house mouse)
C:Date: 16-Sep-1992 #sequence_revision 16-Sep-1992 #text_change 21-Jan-2000
C:Accession: PL0263
R;Shlomchik, M.; Macelli, M.; Shan, H.; Radic, M.Z.; Pisetsky, D.; Marshak-Rothstein, A.
J. Exp. Med. 171, 265-297, 1990
A:Title: Anti-DNA antibodies from autoimmune mice arise by clonal expansion and somatic
A:Reference number: PL0231; MUID:90111618; PMID:2104919
A:Accession: PL0263
A:Molecule type: mRNA
A:Residues: 1-113 <SHL>
A:Cross-references: UNIPARC:UPI0000176AF7
C:Superfamily: immunoglobulin V region; immunoglobulin homology
C:Keywords: heterotrimer; immunoglobulin
F;1-23/Region: framework 1
F;16-96/Domain: immunoglobulin homology <IMM>
F;24-40/Region: complementarity-determining 1
F;41-55/Region: framework 2
F;56-62/Region: complementarity-determining 2
F;63-94/Region: framework 3
F;95-103/Region: complementarity-determining 3
F;104-113/Region: framework 4

Query Match 84.0%; Score 509; DB 2; Length 113;
Best Local Similarity 86.7%; Pred. No. 5.8e-38;
Matches 98; Conservative 5; Mismatches 10; Indels 0; Gaps 0;

QY 4 DIVMTQSPSSLSVAGEKVTMSCKSSQSLNSGNQKNYLAWYQKPGQPPKLLIYGVFIR 63
DB 1 DIVMTQSPSSLSVAGEKVTMSCKSSQSLNSGNQKNYLAWYQKPGQPPKLLIYWASTR 60

QY 64 DSGVPRFTGSGSGTDTLTITSSVQAEADLAVVYQNDHIIYPYTFGGG 116
DB 61 ESGVPRFTGSGSGTDTLTITSSVQAEADLAVVYQNDHIIYPYTFGGG 113

RESULT 9
D30535
Ig kappa chain V region (7C9) - mouse (fragment)
C:Species: Mus musculus (house mouse)
C:Date: 23-Feb-1989 #sequence_revision 23-Feb-1989 #text_change 16-Aug-1996
C:Accession: D30535
R;Claflin, J.L.; Berry, J.; Flaherty, D.; Dunnick, W.
J. Immunol. 138, 3060-3068, 1987
A:Title: Somatic evolution of diversity among anti-phosphocholine antibodies induced with J. Immunol. 138, 3060-3068, 1987
A:Reference number: A30556; MUID:87196439; PMID:3106498
A:Accession: D30535
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-107 <CLA>
A:Cross-references: UNIPARC:UPI0000176AF9
A:Note: the sequence was determined from the differentiated gene
C:Superfamily: immunoglobulin V region; immunoglobulin homology
C:Keywords: heterotrimer; immunoglobulin

Query Match 83.8%; Score 508; DB 2; Length 107;
Best Local Similarity 91.6%; Pred. No. 6.7e-38;
Matches 98; Conservative 1; Mismatches 8; Indels 0; Gaps 0;

QY 4 DIVMTQSPSSLSVAGEKVTMSCKSSQSLNSGNQKNYLAWYQKPGQPPKLLIYGVFIR 63
DB 1 DIVMTQSPSSLSVAGEKVTMSCKSSQSLNSGNQKNYLAWYQKPGQPPKLLIYGASTR 60

QY 64 DSGVPRFTGSGSGTDTLTITSSVQAEADLAVVYQNDHIIYPYTFGGG 110
DB 61 ESGVPRFTGSGSGTDTLTITSSVQAEADLAVVYQNDHSYPLTFGAG 107

RESULT 10
B30535
Ig kappa chain V region (5C8) - mouse (fragment)
C:Species: Mus musculus (house mouse)
C:Date: 23-Feb-1989 #sequence_revision 23-Feb-1989 #text_change 21-Jan-2000
C:Accession: B30535
R;Claflin, J.L.; Berry, J.; Flaherty, D.; Dunnick, W.
J. Immunol. 138, 3060-3068, 1987
A:Title: Somatic evolution of diversity among anti-phosphocholine antibodies induced with J. Immunol. 138, 3060-3068, 1987
A:Reference number: A30556; MUID:87196439; PMID:3106498
A:Accession: B30535
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-107 <CLA>
A:Cross-references: UNIPARC:UPI0000176AF5
A:Note: the sequence was determined from the differentiated gene
C:Superfamily: immunoglobulin V region; immunoglobulin homology
C:Keywords: heterotrimer; immunoglobulin
F;16-96/Domain: immunoglobulin homology <IMM>

Query Match 83.8%; Score 508; DB 2; Length 107;
Best Local Similarity 90.7%; Pred. No. 6.7e-38;
Matches 97; Conservative 2; Mismatches 8; Indels 0; Gaps 0;

QY 4 DIVMTQSPSSLSVAGEKVTMSCKSSQSLNSGNQKNYLAWYQKPGQPPKLLIYGVFIR 63
DB 1 DIVMTQSPSSLSVAGEKVTMSCKSSQSLNSGNQKNYLAWYQKPGQPPKLLIYGASTR 60

QY 64 DSGVPRFTGSGSGTDTLTITSSVQAEADLAVVYQNDHIIYPYTFGGG 110
DB 61 ESGVPRFTGSGSGTDTLTITSSVQAEADLAVVYQNDHSYPLTFGAG 107

RESULT 11
C30535
Ig kappa chain V region (2B2) - mouse (fragment)
C:Species: Mus musculus (house mouse)
C:Date: 23-Feb-1989 #sequence_revision 23-Feb-1989 #text_change 21-Jan-2000
C:Accession: C30535
R;Claflin, J.L.; Berry, J.; Flaherty, D.; Dunnick, W.

J. Immunol. 138, 3060-3068, 1987
A:Title: Somatic evolution of diversity among anti-phosphocholine antibodies induced with A:Reference number: A30556; MUID:87196439; PMID:3106498
A:Accession: C30535
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-105 <CLA>
A:Cross-references: UNIPARC:UPI0000176AF4
A>Note: the sequence was determined from the differentiated gene
C:Superfamily: immunoglobulin V region; immunoglobulin homology
C:Keywords: heterotetramer; immunoglobulin
F:16-96/Domain: immunoglobulin homology <IMM>

Query Match 83.0%; Score 503; DB 2; Length 105;
Best Local Similarity 91.4%; Pred. No. 1.8e-37;
Matches 96; Conservative 2; Mismatches 7; Indels 0; Gaps 0;

QY 4 DIVMTQSPSSLSVSGAGEKVTMSCKSSQSLNRSNKNYLAHYQKPGQPPKLLIYGVFIR 63
Db 1 DIVMTQSPSSLSVSGAGKVTMSCKSSQSLNRSNKNYLAHYQKPGQPPKLLIYGASTR 60

QY 64 DSGVPDRFTGSGSGTDFLTITSSVQAEDLAVYVCQNDHIYPYTFG 108
Db 61 ESGVPDRFTGSGSGTDFLTITSSVQAEDLAVYVCQNDHIYPLTFG 105

RESULT 12
A31790
Ig kappa chain V region (37/9) - mouse
C:Species: Mus musculus (house mouse)
C:Date: 31-Mar-1990 #sequence_revision 31-Mar-1990 #text_change 21-Jan-2000
C:Accession: A31790
R:Schulze-Gahmen, U.; Rini, J.M.; Arevalo, J.; Stura, E.A.; Kenten, J.H.; Wilson, I.A.
J. Biol. Chem. 263, 17100-17105, 1988
A:Title: Preliminary crystallographic data, primary sequence, and binding data for an A:Reference number: A92686; MUID:89034213; PMID:3182835
A:Accession: A31790
A:Molecule type: mRNA
A:Residues: 1-220 <SCH>
A:Cross-references: UNIPARC:UPI0000114E12; GB:M23626; GB:J04061; NID:G533234; PIDN:AAA39
C:Superfamily: immunoglobulin V region; immunoglobulin homology
C:Keywords: heterotetramer; immunoglobulin
F:16-96/Domain: immunoglobulin homology <IMM>

Query Match 81.7%; Score 495; DB 2; Length 220;
Best Local Similarity 84.1%; Pred. No. 1.9e-36;
Matches 95; Conservative 6; Mismatches 12; Indels 0; Gaps 0;

QY 4 DIVMTQSPSSLSVSGAGEKVTMSCKSSQSLNRSNKNYLAHYQKPGQPPKLLIYGVFIR 63
Db 1 DIVMTQSPSSLVTAGKVTMSTSSQSLFNSGKQKNYLTWYQKPGQPPKLLIYWASTR 60

QY 64 DSGVPDRFTGSGSGTDFLTITSSVQAEDLAVYVCQNDHIYPYTFG 116
Db 61 ESGVPDRFTGSGSGTDFLTITSSVQAEDLAVYVCQNDIYNPLTFGGGKLEIK 113

RESULT 13
S68212
Ig kappa chain (Mab03-1) - mouse (fragment)
C:Species: Mus musculus (house mouse)
C:Date: 29-Jul-1997 #sequence_revision 29-Aug-1997 #text_change 11-Jan-2000
C:Accession: S68212
R:Itakagi, M.; Kohda, K.; Hamuro, T.; Harada, A.; Yanaguchi, H.; Imanaka, T.
FEBS Lett. 375, 273-276, 1995
A:Title: Thermostable peroxidase activity with a recombinant antibody L chain-porphyrin A:Reference number: S68211; MUID:96085223; PMID:7498516
A:Accession: S68212
A:Status: preliminary; nucleic acid sequence not shown
A:Molecule type: mRNA
A:Residues: 1-214 <TAK>
A:Cross-references: UNIPARC:UPI000017697E; EMBL:D29668
C:Superfamily: immunoglobulin V region; immunoglobulin homology

Query Match 80.0%; Score 485; DB 2; Length 214;
Best Local Similarity 82.3%; Pred. No. 1.4e-35;
Matches 93; Conservative 8; Mismatches 12; Indels 0; Gaps 0;

QY 4 DIVMTQSPSSLSVSGAGEKVTMSCKSSQSLNRSNKNYLAHYQKPGQPPKLLIYGVFIR 63
Db 1 DIVMTQSPSSLSVSGKVTMSCKSSQSLNRSNKNYLAHYQKPGQPPKLLIYFASSTR 60

QY 64 DSGVPDRFTGSGSGTDFLTITSSVQAEDLAVYVCQNDHIYPYTFG 116
Db 61 ESGVPDRFTGSGSGTDFLTITSSVQAEDLAVYFCQGHYSTPYTFGGGKLEIK 113

RESULT 14
S43103
Ig kappa chain V-J region (4B1 VL) - mouse (fragment)
C:Species: Mus musculus (house mouse)
C:Date: 06-Feb-1995 #sequence_revision 06-Feb-1995 #text_change 24-May-2001
C:Accession: S43103
R:Gilbert, D.; Brard, F.; Margairite, C.; Delpuch, A.; Tron, F.
submitted to the EMBL Data Library, March 1994
A:Description: An idiotype D23-bearing polyclonal, murine anti-DNA monoclonal antibody A:Reference number: S42484
A:Accession: S43103
A:Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-112 <GIL>
A:Cross-references: UNIPARC:UPI0000116626; EMBL:Z31353; NID:G467574; PIDN:CAA83231.1; PII C:Superfamily: immunoglobulin V region; immunoglobulin homology
C:Keywords: heterotetramer; immunoglobulin
F:16-96/Domain: immunoglobulin homology <IMM>

Query Match 78.1%; Score 473.5; DB 2; Length 112;
Best Local Similarity 84.1%; Pred. No. 7.5e-35;
Matches 95; Conservative 6; Mismatches 11; Indels 1; Gaps 1;

QY 4 DIVMTQSPSSLSVSGAGEKVTMSCKSSQSLNRSNKNYLAHYQKPGQPPKLLIYGVFIR 63
Db 1 DIVMTQSPSSLSVSGAGEKVTMSCKSSQSLNRSNKNYLAHYQKPGQPPKLLIYWASTR 60

QY 64 DSGVPDRFTGSGSGTDFLTITSSVQAEDLAVYVCQNDHIYPYTFG 116
Db 61 ESGVPDRFTGSGSGTDFLTITSSVQAEDLAVYVCQSYNL-RTFGGKLEIK 112

RESULT 15
PT0407
Ig light chain V region (S107/VH11 group 1-4) - mouse (fragment)
C:Species: Mus musculus (house mouse)
C:Date: 30-Sep-1993 #sequence_revision 30-Sep-1993 #text_change 21-Jan-2000
C:Accession: PT0407
R:Behar, S.M.; Lustgarten, D.L.; Corbet, S.; Scharff, M.D.
J. Exp. Med. 173, 731-741, 1991
A:Title: Characterization of somatically mutated S107 VH11-encoded anti-DNA autoantibodie A:Reference number: PT0376; MUID:91147903; PMID:1900082
A:Accession: PT0407
A:Molecule type: DNA
A:Residues: 1-113 <BEH>
A:Cross-references: UNIPARC:UPI0000176A05
C:Superfamily: immunoglobulin V region; immunoglobulin homology
C:Keywords: immunoglobulin
F:16-96/Domain: immunoglobulin homology <IMM>

Query Match 78.1%; Score 473.5; DB 2; Length 113;
Best Local Similarity 83.2%; Pred. No. 7.6e-35;
Matches 94; Conservative 7; Mismatches 11; Indels 1; Gaps 1;

QY 4 DIVMTQSPSSLSVSGAGEKVTMSCKSSQSLNRSNKNYLAHYQKPGQPPKLLIYGVFIR 63
Db 1 DIVMTQSPSSLSVSGAGEKVTMSCKSSQSLNRSNKNYLAHYQKPGQPPKLLIYWASTR 60

QY 64 DSGVPDRFTGSGSGTDFLTITSSVQAEDLAVYVCQNDHIYPYTFG 116

Db : ||||| : |||||
61 ECGPDRFTGSGGTDFTLTSSVQAEIDLAVYCKOSYNL-YTFGGGKLEIK 112

Search completed: May 19, 2006, 17:47:24
Job time : 23.0952 secs

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November 2005

Published_Applications Nucleic Acid and Published_Applications Amino Acid database searches now generate two sets of results each. The Published_Applications databases have been split into two parts to reduce the amount of time required for their daily updates. This results in more machine time being available for processing searches.

Newly published applications will appear in the Published_Applications_New databases; older published applications make up the Published_Applications_Main databases.

Searches run against Nucleic Acid Published_Applications produce two sets of results, with the extensions **.rnpbm** (Published_Applications_NA_Main) and **.rnpbn** (Published_Applications_NA_New). Searches run against Amino Acid Published_Applications produce two sets of results, with the extensions **.rapbm** (Published_Applications_AA_Main) and **.rapbn** (Published_Applications_AA_New).

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GenCore version 5.1.8
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OM protein - protein search, using sw model

Run on: May 19, 2006, 17:34:57 ; Search time 176.762 Seconds
(without alignments)
607.041 Million cell updates/sec

Title: US-09-889-936A-8
Perfect score: 606
Sequence: 1 SRGDIWTQSPSSLSVSAGE.....CONDHIVPTFGGKLEIK 116

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 2849598 seqs, 925015592 residues

Total number of hits satisfying chosen parameters: 2849598

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Uniprot_7.2.*
1: uniprot_sprot.*
2: uniprot_trembl.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	531	87.6	255	2 Q6KB05_MOUSE	Q6KB05 mus musculus
2	468	77.2	240	2 Q52164_MOUSE	Q52164 mus musculus
3	456	75.2	114	1 KV4A_HUMAN	P01625 homo sapien
4	454	74.9	134	1 KV4C_HUMAN	P06314 homo sapien
5	452.5	74.7	133	1 KV4B_HUMAN	P06313 homo sapien
6	410	67.7	121	1 KV4O_HUMAN	P06312 homo sapien
7	402	66.3	136	1 KV5B_MOUSE	P01634 mus musculus
8	401	66.2	109	1 KV4D_HUMAN	P83593 homo sapien
9	398	65.7	114	1 KV1A_MOUSE	P01632 mus musculus
10	391	64.5	115	2 Q5F210_MOUSE	Q5F210 mus musculus
11	385	63.5	149	1 KV5A_MOUSE	P01633 mus musculus
12	382.5	63.1	109	2 Q9UL78_HUMAN	Q9UL78 homo sapien
13	381.5	63.0	129	1 KV3L_HUMAN	P18135 homo sapien
14	381.5	63.0	239	2 Q58E08_MOUSE	Q58E08 mus musculus
15	380.5	62.8	129	1 KV3H_HUMAN	P04207 homo sapien
16	380	62.7	236	2 Q6GMX8_HUMAN	Q6GMX8 homo sapien
17	378.5	62.5	129	1 KV3M_HUMAN	P18136 homo sapien
18	376.5	62.1	235	2 Q6GMV9_HUMAN	Q6GMV9 homo sapien
19	376.5	62.1	235	2 Q6GMW0_HUMAN	Q6GMW0 homo sapien
20	374.5	61.8	248	2 Q65ZQ7_MOUSE	Q65ZQ7 mus sp. b3
21	374	61.7	236	2 Q6PIL8_HUMAN	Q6PIL8 homo sapien
22	374	61.7	240	2 Q6PIH6_HUMAN	Q6PIH6 homo sapien
23	373.5	61.6	109	1 KV3B_HUMAN	P01620 homo sapien
24	373	61.6	111	2 Q920E9_MOUSE	Q920E9 mus musculus
25	372.5	61.5	109	1 KV3F_HUMAN	P01624 homo sapien
26	372	61.4	108	1 KV1M_HUMAN	P01605 homo sapien
27	371	61.2	108	1 KV1Y_HUMAN	P80362 homo sapien
28	371	61.2	111	1 KV3H_MOUSE	P01660 mus musculus
29	370.5	61.1	108	1 KV2A_HUMAN	P01619 homo sapien
30	370	61.1	108	1 KV5P_MOUSE	P01649 mus musculus
31	370	61.1	108	2 Q9UL70_HUMAN	Q9UL70 homo sapien

32	370	61.1	115	1 KV2A_HUMAN	P01614 homo sapien
33	369	60.9	108	2 Q8VIJ0_MOUSE	Q8VIJ0 mus musculus
34	369	60.9	236	2 Q6GMW1_HUMAN	Q6GMW1 homo sapien
35	368.5	60.8	219	2 Q65ZC0_MOUSE	Q65ZC0 mus musculus
36	368	60.7	236	2 Q723Y4_HUMAN	Q723Y4 homo sapien
37	367.5	60.6	113	1 KV2G_MOUSE	P01631 mus musculus
38	367	60.6	108	2 Q9UL79_HUMAN	Q9UL79 homo sapien
39	367	60.6	108	2 Q9UL83_HUMAN	Q9UL83 homo sapien
40	367	60.6	111	1 KV3M_MOUSE	P01665 mus musculus
41	367	60.6	131	1 KV3I_MOUSE	P01661 mus musculus
42	367	60.6	238	2 Q66J57_MOUSE	Q66J57 mus musculus
43	366.5	60.5	239	2 Q8NEK0_HUMAN	Q8NEK0 homo sapien
44	366	60.4	108	1 KV1V_HUMAN	P04430 homo sapien
45	365.5	60.3	109	2 Q9UL85_HUMAN	Q9UL85 homo sapien

ALIGNMENTS

RESULT 1
Q6KB05_MOUSE PRELIMINARY; PRT; 255 AA.
AC Q6KB05_MOUSE
DT 05-JUL-2004, integrated into UniProtKB/TrEMBL.
DT 05-JUL-2004, sequence version 1.
DE ScFv B8E5 protein (Fragment).
DE ScFv B8E5 protein (Fragment).
GN Name=scFv B8E5;
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
OC Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=Balb/c;
RX PubMed=15485827; DOI=10.1074/jbc.M407213200;
RA Peter J.C., Wallukat G., Tugler J., Maurice D., Roegel J.C.,
RA Briand J.P., Hoebeke J.;
RT "Modulation of the M2 muscarinic acetylcholine receptor activity with
monoclonal anti-M2 receptor antibody fragments.";
RL J. Biol. Chem. 279:55697-55706(2004).
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EMBL: AJ746180; CAG34081.1; -; Other_DNA.
HSSP; P01837; 1KCR.
DR InterPro; IPR003599; Ig.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003596; Ig V.
DR InterPro; IPR013106; V-set.
DR SMART; SM00409; IG; 2.
DR SMART; SM00406; IGV; 2.
DR PROSITE; PS50835; IG_LIKE; 2.
KW Immunoglobulin domain.
FT NON_TER 1
SQ SEQUENCE 255 AA; 27445 MW; B68BD3835DF713B CRC64;

Query Match 87.6%; Score 531; DB 2; Length 255;
Best Local Similarity 91.2%; Pred. No. 2.4e-48;
Matches 103; Conservative 1; Mismatches 9; Indels 0; Gaps 0;

QY	4	DIVMTQSPSSLSVSAGEKVTMSCKSSQSLNRSNKNYLAWYQKPGQPPKLLIYGVFTR	63
Db	137	DIVMAQSPSSLSVSAGEKVTMSCKSSQSLNRSNKNYLAWYQKPGQPPKLLIYGASTR	196
QY	64	DSGVDRFTGSGSGDFTLTITSSVQAEADLVVYQNDHIYPYTFGGGTGLEIK	116
Db	197	ESGVDRFTGSGSGDFTLTITSSVQAEADLVVYQNDHSYPLTFGAGTGLEIK	249

RESULT 2

```
Q52L64_MOUSE PRELIMINARY; PRT; 240 AA.
ID Q52L64_MOUSE integrated into UniProtKB/TrEMBL.
AC Q52L64;
DT 24-MAY-2005, sequence version 1.
DT 07-FEB-2006, entry version 10.
DE Hypothetical protein.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
OC Muridea; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]_TaxID=10090;
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=Mix FVB/N; TISSUE=Mammary tumor. WAP-TGF alpha model. 7 months
old;
RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA Straube R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shennan C.M., Schuler G.D.,
RA Altschul S.F., Zeeb B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Diatchenko L., Maruina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Huiyk S.W.,
RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahey J., Helton E., Kettner M., Madan A., Rodriguez S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
RA Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smalhus D.E.,
RA Scherch A., Schein J.E., Jones S.J.M., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human
and mouse cDNA sequences.";
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN [2]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=Mix FVB/N; TISSUE=Mammary tumor. WAP-TGF alpha model. 7 months
old;
RG NIH MGC Project;
RL Submitted (APR-2005) to the EMBL/GenBank/DBJ databases.
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EMBL; BC094049; AAH94049.1; -; mRNA.
DR InterPro; IPR003599; Ig.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003597; Ig.C1.
DR InterPro; IPR003006; Ig.MHC.
DR InterPro; IPR003596; Ig.V.
DR Pfam; PF07654; C1-set; 1.
DR SMART; SM00409; Ig; 1.
DR SMART; SM00407; IGc1; 1.
DR SMART; SM00406; Igv; 1.
DR PROSITE; PS50835; IG LIKE; 2.
DR PROSITE; PS00290; IG MHC; UNKNOWN_1.
KW Hypothetical protein.
SQ SEQUENCE 240 AA; 26609 MW; CF6630CCC002E52C CRC64;

Query Match 77.2%; Score 468; DB 2; Length 240;
Best Local Similarity 78.9%; Pred. No. 1.3e-41;
Matches 90; Conservative 10; Mismatches 14; Indels 0; Gaps 0;

Qy 3 GDVMTQSPSSLSVSGEKVTMSCKSSQSLNSRNQKNVLAWYQKQPGPPKLLIYGVFI 62
Db 20 GDVMTQSPSSLSVSGEKVTMSCKSSQSLNSRNQKNVLAWYQKQPGPPKLLIYWAST 79

Qy 63 RDSGVPDRFTSGSGGTDFLTLTSSVQAEALVYVYQNDHIYPTFGGTGKLEIK 116
Db 80 RESGVPDRFTSGSGGTDFLTLTSSVQAEALVYVYQNDHIYPTFGGTGKLEIK 133
```

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FT  STRAND      36      37
FT  STRAND      39      44
FT  TURN        46      47
FT  STRAND      48      48
FT  STRAND      51      55
FT  TURN        56      58
FT  STRAND      59      60
FT  TURN        62      63
FT  STRAND      66      67
FT  TURN        68      73
FT  STRAND      74      75
FT  TURN        76      83
FT  STRAND      86      88
FT  TURN        90      96
FT  STRAND      98      101
FT  STRAND     103      104
FT  STRAND     108      112
SQ  SEQUENCE  114 AA; 12640 MW; 0647FD1D17F236485 CRC64;

Query Match      75.2%; Score 456; DB 1; Length 114;
Best Local Similarity 77.0%; Pred. No. 1e-40;
Matches 87; Conservative 11; Mismatches 15; Indels 0; Gaps 0;

QY  4 DIVMTQSPSSLSVAGEKVTMSCKSSQSLNSRNQKNYLAWYQKPGQPPKLLIYGVFIR 63
DB  1 DIVMTQSPDLSAVSLGERATINCKSSQSVLYSSNKNYLAWYQKPGQPPKLLIYWASTR 60
QY  64 DSGVDPDRFTGSGSGTDFTLTITSSVOAEDLAVYYCQNDHIYPYTFGGGTGLEIK 116
DB  61 ESGVDPDRFSGSGSGTDFTLTITSSLOAEDVAVYCCQYYSTPYTFSGGTGLEIK 113

RESULT 4
KV4C HUMAN
ID  KV4C_HUMAN STANDARD; PRT; 134 AA.
AC  P06314;
DT  01-JAN-1988, integrated into UniProtKB/Swiss-Prot.
DT  01-APR-1988, sequence version 1.
DT  07-NAR-2006, entry version 45.
DE  Ig kappa chain V-IV region B17 precursor.
OS  Homo sapiens (Human)
OC  Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC  Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;
OC  Homo.
OX  NCBI_TaxID=9606;
RN  [1]
RP  NUCLEOTIDE SEQUENCE [MRNA].
RX  MEDLINE=86041854; PubMed=2997713;
RA  Marsh P., Mills F., Gould H.;
RT  "Detection of a unique human V kappa IV germline gene by a cloned cDNA
RT  probe.";
RL  Nucleic Acids Res. 13:6531-6544 (1985).
RN  [2]
RP  SEQUENCE REVISION TO 76.
RA  Marsh P.;
RL  Submitted (OCT-1986) to the EMBL/GenBank/DBJ databases.
CC  Copyrighted by the UniProt Consortium, see http://www.uniprot.org/terms
CC  Distributed under the Creative Commons Attribution-NoDerivs License
CC  -----
DR  EMBL; X02990; CAA26733.1; -; mRNA.
DR  HSSP; P01625; 1LVE.
DR  SMR; P06314; 21-134.
DR  LinkHub; P06314; -.
DR  GO; GO:0005576; C:extracellular region; NAS.
DR  GO; GO:0003823; F:antigen binding; NAS.
DR  GO; GO:0006955; P:immune response; NAS.
DR  InterPro; IPR003599; IG.
DR  InterPro; IPR007110; IG-like.
DR  InterPro; IPR003596; IG_v.
DR  InterPro; IPR013106; V-set.
DR  Pfam; PF07686; V-set; 1.
DR  SMART; SM00409; IG; 1.

QY  3 GDIVMTQSPSSLSVAGEKVTMSCKSSQSLNSRNQKNYLAWYQKPGQPPKLLIYGVFI 62
DB  20 GDIVMTQSPDLSAVSLGERATINCKSSQSVLYSSNKNYLAWYQKPGQPPKLLIYWAST 79
QY  63 RDSGVDPDRFTGSGSGTDFTLTITSSVOAEDLAVYYCQNDHIYPYTFGGGTGLEIK 116
DB  80 RESGVDPDRFSGSGSGTDFTLTITSSLOAEDVAVYCCQYYNLPWTFGGTKVBIK 133

RESULT 5
KV4B HUMAN
ID  KV4B_HUMAN STANDARD; PRT; 133 AA.
AC  P06313;
DT  01-JAN-1988, integrated into UniProtKB/Swiss-Prot.
DT  01-JAN-1988, sequence version 1.
DT  07-MAR-2006, entry version 43.
DE  Ig kappa chain V-IV region JI precursor.
OS  Homo sapiens (Human)
OC  Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC  Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;
OC  Homo.
OX  NCBI_TaxID=9606;
RN  [1]
RP  NUCLEOTIDE SEQUENCE [GENOMIC DNA].
RX  MEDLINE=86041853; PubMed=2997712;
RA  Klobeck H.G., Bornkamm G.W., Combrato G., Mocikat R., Pohlenz H.D.,
RA  Zachau H.G.;
RT  "Subgroup IV of human immunoglobulin K light chains is encoded by a
RT  single germline gene.";
RL  Nucleic Acids Res. 13:6515-6529 (1985).
CC  Copyrighted by the UniProt Consortium, see http://www.uniprot.org/terms
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CC  -----
DR  EMBL; Z00022; CAA77317.1; -; Genomic_DNA.
DR  PIR; A01904; K4HUJ1.
DR  HSSP; P01625; 1LVE.
DR  SMR; P06313; 21-133.
DR  GO; GO:0005576; C:extracellular region; NAS.
DR  GO; GO:0003823; F:antigen binding; NAS.
DR  GO; GO:0006955; P:immune response; NAS.
DR  InterPro; IPR003599; IG.
DR  InterPro; IPR007110; IG-like.
DR  InterPro; IPR003596; IG_v.
DR  InterPro; IPR013106; V-set.
DR  Pfam; PF07686; V-set; 1.
DR  SMART; SM00409; IG; 1.
DR  PROSITE; PS00835; IG LIKE; 1.
KW  Immunoglobulin domain; Immunoglobulin V region; Signal.
FT  SIGNAL      1      20
FT  CHAIN       21      133

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DR  SMART; SM00406; IGv; 1.
DR  PROSITE; PS00835; IG LIKE; 1.
KW  Immunoglobulin domain; Immunoglobulin V region; Signal.
FT  SIGNAL      1      20
FT  CHAIN       21      134
FT  REGION      21      43
FT  REGION      44      60
FT  REGION      61      75
FT  REGION      76      82
FT  REGION      83      114
FT  REGION      115      121
FT  REGION      122      133
FT  DISULFID     43      114
FT  NON_TER     134      134
SQ  SEQUENCE  134 AA; 14966 MW; 6413A22FD0738832 CRC64;

Query Match      74.9%; Score 454; DB 1; Length 134;
Best Local Similarity 75.4%; Pred. No. 2.1e-40;
Matches 86; Conservative 13; Mismatches 15; Indels 0; Gaps 0;

QY  3 GDIVMTQSPSSLSVAGEKVTMSCKSSQSLNSRNQKNYLAWYQKPGQPPKLLIYGVFI 62
DB  20 GDIVMTQSPDLSAVSLGERATINCKSSQSVLYSSNKNYLAWYQKPGQPPKLLIYWAST 79
QY  63 RDSGVDPDRFTGSGSGTDFTLTITSSVOAEDLAVYYCQNDHIYPYTFGGGTGLEIK 116
DB  80 RESGVDPDRFSGSGSGTDFTLTITSSLOAEDVAVYCCQYYNLPWTFGGTKVBIK 133

RESULT 5
KV4B HUMAN
ID  KV4B_HUMAN STANDARD; PRT; 133 AA.
AC  P06313;
DT  01-JAN-1988, integrated into UniProtKB/Swiss-Prot.
DT  01-JAN-1988, sequence version 1.
DT  07-MAR-2006, entry version 43.
DE  Ig kappa chain V-IV region JI precursor.
OS  Homo sapiens (Human)
OC  Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC  Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;
OC  Homo.
OX  NCBI_TaxID=9606;
RN  [1]
RP  NUCLEOTIDE SEQUENCE [GENOMIC DNA].
RX  MEDLINE=86041853; PubMed=2997712;
RA  Klobeck H.G., Bornkamm G.W., Combrato G., Mocikat R., Pohlenz H.D.,
RA  Zachau H.G.;
RT  "Subgroup IV of human immunoglobulin K light chains is encoded by a
RT  single germline gene.";
RL  Nucleic Acids Res. 13:6515-6529 (1985).
CC  Copyrighted by the UniProt Consortium, see http://www.uniprot.org/terms
CC  Distributed under the Creative Commons Attribution-NoDerivs License
CC  -----
DR  EMBL; Z00022; CAA77317.1; -; Genomic_DNA.
DR  PIR; A01904; K4HUJ1.
DR  HSSP; P01625; 1LVE.
DR  SMR; P06313; 21-133.
DR  GO; GO:0005576; C:extracellular region; NAS.
DR  GO; GO:0003823; F:antigen binding; NAS.
DR  GO; GO:0006955; P:immune response; NAS.
DR  InterPro; IPR003599; IG.
DR  InterPro; IPR007110; IG-like.
DR  InterPro; IPR003596; IG_v.
DR  InterPro; IPR013106; V-set.
DR  Pfam; PF07686; V-set; 1.
DR  SMART; SM00409; IG; 1.
DR  PROSITE; PS00835; IG LIKE; 1.
KW  Immunoglobulin domain; Immunoglobulin V region; Signal.
FT  SIGNAL      1      20
FT  CHAIN       21      133

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FT REGION 64 78 Framework-2.
FT REGION 79 85 Complementarity-determining-2.
FT REGION 86 117 Framework-3.
FT REGION 118 126 Complementarity-determining-3.
FT REGION 127 136 Framework-4.
FT NON_TER 136 136
FT STRAND 34 36
FT STRAND 38 38
FT STRAND 41 43
FT STRAND 44 45
FT STRAND 48 53
FT STRAND 55 56
FT STRAND 59 60
FT TURN 62 67
FT TURN 69 70
FT STRAND 71 71
FT STRAND 74 78
FT STRAND 79 81
FT STRAND 82 83
FT TURN 85 86
FT TURN 89 90
FT STRAND 93 95
FT STRAND 97 106
FT STRAND 109 109
FT TURN 110 111
FT STRAND 113 119
FT STRAND 121 124
FT STRAND 126 127
SQ SEQUENCE 136 AA; 14902 MW; 8CDD85113996D1C2 CRC64;

Query Match 66.3%; Score 402; DB 1; Length 136;
Best Local Similarity 67.5%; Pred. No. 8e-35;
Matches 77; Conservative 16; Mismatches 15; Indels 6; Gaps 1;

QY 3 GDVMTQSPSSLSVSAGEKVTMSCKSSQSLNSRNQKNYLAWYQOKPGQPPKLLIYGVFI 62
Db 29 GNIVMTQSPKSMVSMGERTVITCKASENVV-----TVVSWYQOKPEQSPKLLIYGASN 82

QY 63 RDSGVDPDRFTGSGSGDFTLTITSSVQAEADLAVYQNDHIYPYTFGGGKLEIK 116
Db 83 RYTGVPDRFTGSGSATDFTLTITSSVQAEADLADYHCQGYSPYPTFGGKLEIK 136

RESULT 8
KV4D HUMAN STANDARD; PRT; 109 AA.
AC P83593;
DT 30-MAY-2003, integrated into UniProtKB/Swiss-Prot.
DT 07-MAR-2006, sequence version 1.
DE Ig kappa chain V-IV region STH (Fragment).
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;
OC Homo.
OX NCBI_TaxID=9606;
RN [1]
RP TISSUE=Abdominal adipose tissue;
RX MEDLINE=98249779; PubMed=9588180; DOI=10.1006/bbrc.1998.8515;
RA Olsen K.E., Sletten K., Westermark P.;
RT "Extended analysis of AL-amyloid protein from abdominal wall
RT subcutaneous fat biopsy: kappa IV immunoglobulin light chain.";
RL Biochem. Biophys. Res. Commun. 245:713-716(1998).
CC -!- FUNCTION: May play an important role in fibrillogenesis.
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CC
CC
DR SMR; P83593; 1-109.
DR InterPro; IPR003599; Ig.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003596; Ig_v.

DR InterPro; IPR013106; V-set.
DR Pfam; PF07686; V-set; 1.
DR SMART; SM00409; IG; 1.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PS00835; IG LIKE; 1.
KW Direct protein sequencing; Immunoglobulin domain;
KW Immunoglobulin V region.
FT CHAIN 1 >109
Ig kappa chain V-IV region STH.
/FTID=PRO_0000059769.
FT REGION 1 23 Framework-1.
FT REGION 24 40 Complementarity-determining-1.
FT REGION 41 55 Framework-2.
FT REGION 56 62 Complementarity-determining-2.
FT REGION 63 94 Framework-3.
FT REGION 95 101 Complementarity-determining-3.
FT REGION 102 109 Framework-4.
FT DISULFID 23 94 By similarity.
FT UNSURE 23 23
FT UNSURE 94 94
FT NON_TER 109 109
FT SEQUENCE 109 AA; 12060 MW; 0C4F31EA11E12A0B CRC64;

Query Match 66.2%; Score 401; DB 1; Length 109;
Best Local Similarity 70.6%; Pred. No. 7.8e-35;
Matches 77; Conservative 10; Mismatches 22; Indels 0; Gaps 0;

QY 4 DIVMTQSPSSLSVSAGEKVTMSCKSSQSLNSRNQKNYLAWYQOKPGQPPKLLIYGVFIR 63
Db 1 DIVMTQSPDSLVSLSGERATINCRSSQSVLYSSNKNYLAWYQOKPGQAPKLLFSWASTR 60

QY 64 DSGVDPDRFTGSGSGDFTLTITSSVQAEADLAVYQNDHIYPYTFGGGK 112
Db 61 ESGVDPDRFTGSGSGDFTLTIPGQAEADVAVYQCYRIPYTFGGQAK 109

RESULT 9
KV1A MOUSE STANDARD; PRT; 114 AA.
ID KV1A MOUSE
AC P01632;
DT 21-JUL-1986, integrated into UniProtKB/Swiss-Prot.
DT 21-JUL-1986, sequence version 1.
DT 07-MAR-2006, entry version 44.
DE Ig kappa chain V-I region S107A.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
OC Muroidea; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP NUCLEOTIDE SEQUENCE [MRNA].
RX MEDLINE=81241357; PubMed=6788890; DOI=10.1084/jem.153.5.1366;
RA Kwan S.-P., Rudikoff S., Seidman J.G., Leder P., Scharff M.D.;
RT "Nucleic acid and protein sequences of phosphocholine-binding light
RT chains.";
RL J. Exp. Med. 153:1366-1370(1981).
RN [2]
RP NUCLEOTIDE SEQUENCE [MRNA] OF 1-113.
RX MEDLINE=89035545; PubMed=3141511;
RA Claflin J.L., Berry J.;
RT "Genetics of the phosphocholine-specific antibody response to
RT Streptococcus pneumoniae. Germ-line but not mutated T15 antibodies are
RT dominantly selected.";
RL J. Immunol. 141:4012-4019(1988).
CC -!- FUNCTION: Anti-phosphocholine antibody.
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CC
CC
DR EMBL; U29423; AAC00033.1; -; mRNA.
DR PIR; A01915; KVM57A.
DR HSP; Q9ER29; 2A2.
DR SMR; P01632; 1-114.
DR InterPro; ENSMUSG000000052500; Mus musculus.

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DR MGI: 3577282; U29423.
DR InterPro; IPR003599; Ig.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003596; Ig_v.
DR InterPro; IPR013106; V-set.
DR Pfam; PF07686; V-set; 1.
DR SMART; SM00409; IG; 1.
DR SMART; SM00406; IGv; 1.
DR PROSITE; PS50835; IG_LIKE; 1.
KW Immunoglobulin domain; Immunoglobulin V region.
FT CHAIN 1 >114
FT /FTID=PRO 0000059770.
FT REGION 1 23
FT REGION 24 40
FT REGION 41 55
FT REGION 56 62
FT REGION 63 94
FT REGION 95 103
FT REGION 104 113
FT REGION 104 113
FT DISULFID 23 94
FT NON_TER 114
SQ SEQUENCE 114 AA; 12717 MW; 32008EC859DBB67B CRC64;

Query Match 65.7%; Score 398; DB 1; Length 114;
Best Local Similarity 68.1%; Pred. No. 1.7e-34;
Matches 77; Conservative 15; Mismatches 21; Indels 0; Gaps 0;

QY 4 DIVMTQSPSSLSVSAAGEKVTWMSCKSSQSLNRSNKNYLAWYQKPGQPPKLLIYGVP 63
Db 1 DIVMTQSPFLAVTASKKVITISCTASESLYSKHKVHYLAWYQKPGQPPKLLIYGASNR 60
QY 64 DSGVPDRFTGSGGTDFTLTITSSVQAEADLAVYVCQNDHIYPTFGGKLEIK 116
Db 61 YIGVPRFTGSGGTDFTLTITSSVQVEDLTHYCAQFYSPLTFTGAGTKLEIK 113

RESULT 10
QSF210 MOUSE
ID QSF210_MOUSE PRELIMINARY; PRT; 115 AA.
AC QSF210;
DT 15-MAR-2005, integrated into UniProtKB/TrEMBL.
DT 15-MAR-2005, sequence version 1.
DE Kappa light chain variable region (Fragment).
GN Name=IgG1 anti-TS1 VH;
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
OC Muridae; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RX MEDLINE=22716456; PubMed=12833571; DOI=10.1002/jmr.617;
RA Erlandsson A., Holm P., Ullen A., Stigbrand T., Sundstrom B.E.;
RT "Studies of the interactions between the anticytoklerin 8 monoclonal
RT antibody TS1, its antigen and its anti-idiotypic antibody alphaTS1";
RL J. Mol. Recognit. 16:157-163 (2003).
RN [2]
RP NUCLEOTIDE SEQUENCE.
RA Erlandsson A.;
RL Submitted (FEB-2005) to the EMBL/GenBank/DBJ databases.
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CC -----
CC EMBL; AJ894575; CAI56337.1; -; mRNA.
DR InterPro; IPR003599; Ig.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003596; Ig_v.
DR InterPro; IPR013106; V-set.
DR SMART; SM00409; IG; 1.
DR SMART; SM00406; IGv; 1.
DR PROSITE; PS50835; IG_LIKE; 1.
DR
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KW Immunoglobulin domain.
FT NON_TER 1
FT NON_TER 115
SQ SEQUENCE 115 AA; 12560 MW; E4D3BF3D63E88007 CRC64;

Query Match 64.5%; Score 391; DB 2; Length 115;
Best Local Similarity 68.4%; Pred. No. 9.9e-34;
Matches 78; Conservative 14; Mismatches 20; Indels 2; Gaps 2;

QY 4 DIVMTQSPSSLSVSAAGEKVTWMSCKSSQSLNRSNKNYLAWYQKPGQPPKLLIYGVP 63
Db 1 DIVMTQSPFLVSLGQASISCRSSQSLVHS-NGNTYLHWYLOKPGQSPKLLIYKVSNR 59
QY 64 DSGVPDRFTGSGGTDFTLTITSSVQAEADLAVYVCQNDHIYPTFGGKLEIK 116
Db 60 FSGVPRFTGSGGTDFTLTITSSVQAEADLGVYFCSTTHVPPYTFGGGKLEMK 113

RESULT 11
KVSA_MOUSE
ID KVSA_MOUSE STANDARD; PRT; 149 AA.
AC P01633;
DT 21-JUL-1986, integrated into UniProtKB/Swiss-Prot.
DT 21-JUL-1986, sequence version 1.
DT 07-MAR-2006, entry version 45.
DE Ig kappa chain V-V region MPC11 precursor.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
OC Muridae; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP NUCLEOTIDE SEQUENCE [GENOMIC DNA] OF 1-71.
RX MEDLINE=83001944; PubMed=6288267; DOI=10.1016/0092-8674(82)90184-2;
RA Kelley D.E., Coleclough C., Perry R.P.;
RT "Functional significance and evolutionary development of the 5'-
RT terminal regions of immunoglobulin variable-region genes.";
RL Cell 29:681-689 (1982).
RN [2]
RP NUCLEOTIDE SEQUENCE [GENOMIC DNA] OF 41-149.
RX MEDLINE=80176554; PubMed=6245773;
RA Rabbitts T.H., Hamlyn P.H., Matthyssens G., Roe B.A.;
RT "The variability, arrangement, and rearrangement of immunoglobulin
RT genes.";
RL Can. J. Biochem. 58:176-187 (1980).
RN [3]
RP PROTEIN SEQUENCE OF 30-149.
RX MEDLINE=78186617; PubMed=418775;
RA Smith G.P.;
RT "Sequence of the full-length immunoglobulin kappa-chain of mouse
RT myeloma MPC 11.";
RL Blochem. J. 171:337-347 (1978).
CC CC
CC -1- MISCELLANEOUS: The mature chain has 12 additional residues at its
CC amino end, due to a tandem duplication of 36 nucleotides after the
CC codon for residue 36. Residue 42 corresponds to the N-terminal
CC residue of typical kappa chains.
CC -----
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CC -----
CC EMBL; J00561; AAA38776.1; -; Genomic DNA.
DR PIR; A90823; KWS11.
DR HSPF; P01634; IIGC.
DR SMR; P01633; 42-149.
DR Ensembl; ENSMUSG000000061362; Mus musculus.
DR InterPro; IPR003599; Ig.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003596; Ig_v.
DR InterPro; IPR013106; V-set.
DR Pfam; PF07686; V-set; 1.
DR SMART; SM00409; IG; 1.
DR SMART; SM00406; IGv; 1.
DR PROSITE; PS50835; IG_LIKE; 1.
DR
```

```

KW Direct protein sequencing; Immunoglobulin domain;
KW Immunoglobulin V region; Repeat; Signal.
FT SIGNAL 1 29
FT CHAIN 30 149 Ig kappa chain V-V region MPC11.
FT 30 149 /FTid=PRO_0000015189.
FT REPEAT 26 35
FT REPEAT 38 47
FT REPEAT 42 64
FT REGION 65 75 Framework-1.
FT REGION 76 90 Complementarity-determining-1.
FT REGION 91 97 Framework-2.
FT REGION 98 129 Complementarity-determining-2.
FT REGION 130 138 Framework-3.
FT REGION 139 148 Complementarity-determining-3.
FT REGION 149 149 Framework-4.
FT NON_TER 149
SQ SEQUENCE 149 AA; 16434 MW; B0480C87B682AC3E CRC64;

Query Match 63.5%; Score 385; DB 1; Length 149;
Best Local Similarity 66.7%; Pred. No. 6e-33;
Matches 76; Conservative 12; Mismatches 20; Indels 6; Gaps 1;

QY 3 GDIVMTQSPSSLSVSAAGEKVTMSCKSSQSLNSRNQKYLAWYQKPGQPPKLLIYGVPF 62
Db 41 GDIVMTQSHKFNSTVGDVRSITCKASQDVSTI-----VAVYQKPGQSPKLLIYSASY 94
QY 63 RDSGVPDRFTGSGGTDFTLTITSSVQAEDLAVYYCQNDHIYPYTFGGGKLEIK 116
Db 95 RYTGVPDRFTGSGGTDFTLTITSSVQAEDLAVYYCQHYSTPTPTFGGKLEIK 148

RESULT 12
Q9UL78 HUMAN PRELIMINARY; PRT; 109 AA.
AC Q9UL78;
DT 01-MAY-2000, integrated into UniProtKB/TrEMBL.
DT 01-MAY-2000, sequence version 1.
DT 07-FEB-2006, entry version 22.
DE Myosin-reactive immunoglobulin light chain variable region (Fragment).
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;
OC Homo.
OX NCBI_TaxID=9606;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RX MEDLINE=92228746; PubMed=1373487;
RA Zebddee S.L., Barbas C.F. 3rd, Hom Y.L., Caothien R.H., Graff R.,
RA DeGraw J., Pyati J., LaPolla R., Burton D.R., Lerner R.A.;
RT "Human combinatorial antibody libraries to hepatitis B surface
RT antigen.";
RL Clin. Immunol. Immunopathol. 87:184-192(1998).
RN [2]
RP NUCLEOTIDE SEQUENCE.
RX MEDLINE=92228746; PubMed=1373487;
RA Zebddee S.L., Barbas C.F. 3rd, Hom Y.L., Caothien R.H., Graff R.,
RA DeGraw J., Pyati J., LaPolla R., Burton D.R., Lerner R.A.;
RT "Human combinatorial antibody libraries to hepatitis B surface
RT antigen.";
RL Proc. Natl. Acad. Sci. U.S.A. 89:3175-3179(1992).
RN [3]
RP NUCLEOTIDE SEQUENCE.
RX MEDLINE=93170387; PubMed=8436174;
RA Wagner S.D., Luzzatto L.;
RT "V kappa gene segments rearranged in chronic lymphocytic leukemia are
RT distributed over a large portion of the V kappa locus and do not show
RT somatic mutation.";
RL Eur. J. Immunol. 23:391-397(1993).
RN [4]
RP NUCLEOTIDE SEQUENCE.
RX MEDLINE=92202880; PubMed=1552291; DOI=10.1084/jem.175.4.983;
RA Martin T., Duffy S.F., Carson D.A., Kipps T.J.;
RT "Evidence for somatic selection of natural autoantibodies.";
RL J. Exp. Med. 175:983-991(1992).

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CC -----
CC EMBL; AF035036; AAD56272.1; -; mRNA.
DR PIR; A30601; A30601.
DR PIR; A30601; A30608.
DR PIR; B30601; B30601.
DR PIR; B30607; B30607.
DR PIR; C30601; C30601.
DR PIR; C30607; C30607.
DR PIR; C30608; C30608.
DR PIR; D30601; D30601.
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DR PIR; I30601; I30601.
DR PIR; PH0963; PH0963.
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DR PIR; S33988; S33988.
DR PIR; S34096; S34096.
DR HSP; P01625; 1EK3.
DR SMR; Q9UL78; 1-109.
DR InterPro; IPR003599; Ig.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003596; Ig.V.
DR InterPro; IPR013106; V-set.
DR SMART; SM00409; IG_1.
DR SMART; SM00406; IGV_1.
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KW Immunoglobulin domain.
FT NON_TER 1
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Best Local Similarity 64.6%; Pred. No. 7.6e-33;
Matches 73; Conservative 17; Mismatches 18; Indels 5; Gaps 1;

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Db 1 EIVLTQSPGTSLSLSPGERATLSCRASQSVSS-----YLAWYQKPGQAPRLIIYGASR 55
QY 64 DSGVDPDRFTGSGGTDFTLTITSSVQAEDLAVYYCQNDHIYPYTFGGGKLEIK 116
Db 56 ATGIDPRFSGSGGTDFTLTISRLEPEDCAVYCYQYGSPLTFGGGTKEIK 108

RESULT 13
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AC P18135;
DT 01-NOV-1990, integrated into UniProtKB/Swiss-Prot.
DT 01-NOV-1990, sequence version 1.
DT 07-MAR-2006, entry version 41.
DE Ig kappa chain V-III region HAH precursor.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;
OC Homo.
OX NCBI_TaxID=9606;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RX MEDLINE=88171307; PubMed=3127527; DOI=10.1084/jem.167.3.840;
RA Kipps T.J., Tomhave E., Chen P.P., Carson D.A.;
RT "Autoantibody-associated kappa light chain variable region gene

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RN  [1]
RP  NUCLEOTIDE SEQUENCE [GENOMIC DNA].
RX  MEDLINE=86177570; PubMed=3083417;
RA  Jirik F.R., Sorge J., Fong S., Heitzmann J.G., Curd J.G., Chen P.P.,
RA  Goldfien R., Carson D.A.;
RT  "Cloning and sequence determination of a human rheumatoid factor
RT  light-chain gene".
RL  Proc. Natl. Acad. Sci. U.S.A. 83:2195-2199(1986).
CC  -----
CC  Copyrighted by the UniProt Consortium, see http://www.uniprot.org/terms
CC  Distributed under the Creative Commons Attribution-NoDerivs License
CC  -----
DR  EMBL; M12740; AA58992.1; -; Genomic_DNA.
DR  HSSP; P01625; ILVE.
DR  SMR; P04207; 21-129.
DR  LinkHub; P04207; -.
DR  GO; GO:0005576; C:extracellular region; NAS.
DR  GO; GO:0003823; F:antigen binding; NAS.
DR  GO; GO:0005955; P:immune response; NAS.
DR  InterPro; IPR003599; Ig.
DR  InterPro; IPR007110; Ig-like.
DR  InterPro; IPR003596; Ig V.
DR  InterPro; IPR013106; V-set.
DR  Pfam; PF07686; V-set; 1.
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DR  SMART; SM00406; IGV; 1.
DR  PROSITE; PS50835; IG LIKE; 1.
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FT  REGION 21 43
FT  REGION 44 54
FT  REGION 55 69
FT  REGION 70 76
FT  REGION 77 108
FT  REGION 109 118
FT  REGION 119 129
FT  DISULFID 43 108
FT  NON_TER 129 129
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      Complementarity-determining-1.
      Framework-2.
      Complementarity-determining-2.
      Framework-3.
      Complementarity-determining-3.
      Jk1 segment.
      By similarity.

Query Match      62.8%; Score 380.5; DB 1; Length 129;
Best Local Similarity 63.5%; Pred. No. 1.5e-32;
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QY  63  RDSGVDPRTGSGSGTDFLTITSSVQAEVLAVVYQNDHIY-PYTFGGGKLEIK 116
DB  74  RATGIPARFSGSGSGTEFTLTISRLQSEDFAVYCCQYNNWPPWTFQGTRVEIK 128

Search completed: May 19, 2006, 17:46:32
Job time : 178.762 secs
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OM protein - protein search, using sw model

Run on: May 19, 2006, 17:46:56 ; Search time 33.6032 Seconds
(without alignments)
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Title: US-09-889-936A-8

Perfect score: 606

Sequence: 1 SRGDIVMTQSPSSLSVSAGE.....QNDRHYPTFGGKLEIK 116

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 650591 seqs, 87530628 residues

Total number of hits satisfying chosen parameters: 650591

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Issued Patents_AA:*

- 1: /EMC_Celerra_SIDS3/ptodata/2/iaa/5 COMB.pcp.*
- 2: /EMC_Celerra_SIDS3/ptodata/2/iaa/6 COMB.pcp.*
- 3: /EMC_Celerra_SIDS3/ptodata/2/iaa/7 COMB.pcp.*
- 4: /EMC_Celerra_SIDS3/ptodata/2/iaa/H COMB.pcp.*
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- 7: /EMC_Celerra_SIDS3/ptodata/2/iaa/backfiles1.pcp.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match %	Length	DB ID	Description
1	541	89.3	113	1	US-08-467-420A-45
2	541	89.3	113	1	US-08-470-110A-45
3	541	89.3	113	1	US-08-667-769A-45
4	541	89.3	113	1	US-08-940-371A-45
5	541	89.3	113	2	US-08-637-647A-45
6	541	89.3	113	2	US-10-700-740A-45
7	541	89.3	113	5	PCT-US95-17082A-45
8	536	88.4	113	1	US-08-077-252B-4
9	536	88.4	113	1	US-08-107-669D-2
10	536	88.4	113	1	US-08-472-788A-2
11	536	88.4	113	1	US-08-477-531B-2
12	536	88.4	113	1	US-08-082-842A-2
13	536	88.4	113	2	US-09-002-753A-4
14	536	88.4	113	2	US-09-657-274A-4
15	536	88.4	113	5	PCT-US94-06687-4
16	536	88.4	115	1	US-07-942-245-7
17	535	88.3	113	1	US-08-467-420A-46
18	535	88.3	113	1	US-08-470-110A-46
19	535	88.3	113	1	US-08-667-769A-46
20	535	88.3	113	1	US-08-940-371A-46
21	535	88.3	113	1	US-08-637-647A-46
22	535	88.3	113	2	US-10-700-740A-46
23	535	88.3	113	5	PCT-US95-17082A-46
24	534	88.1	277	1	US-08-256-790-2
25	528	87.1	113	1	US-08-442-542-12
26	528	87.1	113	2	US-08-765-469-12

27	528	87.1	114	2	US-09-232-290-26	Sequence 26, Appl
28	526	86.8	113	1	US-08-667-769A-16	Sequence 16, Appl
29	526	86.8	113	2	US-10-700-740-16	Sequence 16, Appl
30	526	86.8	113	5	PCT-US95-17082A-16	Sequence 16, Appl
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33	521	86.0	113	2	US-08-765-469-47	Sequence 47, Appl
34	518	85.5	115	2	US-09-561-500-9	Sequence 9, Appl
35	518	85.5	115	2	US-09-561-108-9	Sequence 9, Appl
36	518	85.5	115	2	US-09-561-526-9	Sequence 9, Appl
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41	514	84.8	154	2	US-08-513-968-36	Sequence 36, Appl
42	508	83.8	134	2	US-08-718-323A-4	Sequence 4, Appl
43	508	83.8	134	2	US-09-587-526-4	Sequence 4, Appl
44	505	83.3	354	2	US-09-393-627B-28	Sequence 28, Appl
45	504	83.2	113	1	US-08-467-420A-21	Sequence 21, Appl

ALIGNMENTS

RESULT 1

US-08-467-420A-45
; Sequence 45, Application US/08467420A
; Patent No. 5683892
; GENERAL INFORMATION:
; APPLICANT: Ames, Robert S.
; APPLICANT: Appelbaum, Edward R.
; APPLICANT: Chaiken, Irwin M.
; APPLICANT: Cook, Richard M.
; APPLICANT: Gross, Mitchell S.
; APPLICANT: Holmes, Stephen D.
; APPLICANT: McMillan, Lynette J.
; APPLICANT: Theisen, Timothy W.
; TITLE OF INVENTION: Recombinant IL5 Antagonists Useful in
; NUMBER OF SEQUENCES: 74
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: SmithKline Beecham Corp./Corporate
; ADDRESSEE: Intellectual Property
; STREET: P. O. Box 1539-UM2220
; CITY: King of Prussia
; STATE: Pennsylvania
; COUNTRY: USA
; ZIP: 19406-0939
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/467,420A
; FILING DATE:
; CLASSIFICATION: 536
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/363131
; FILING DATE: 23-DEC-1994
; ATTORNEY/AGENT INFORMATION:
; NAME: Sutton, Jeffrey A.
; REGISTRATION NUMBER: 34,028
; REFERENCE/DOCKET NUMBER: P50282
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 610 270-5024
; TELEFAX: 610 270-5090
; INFORMATION FOR SEQ ID NO: 45:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 113 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear

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; MOLECULE TYPE: protein
US-08-467-420A-45
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Best Local Similarity 91.2%; Pred. No. 2.2e-42;
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RESULT 2
US-08-470-110A-45
; Sequence 45, Application US/08470110A
; Patent No. 5693323
; GENERAL INFORMATION:
; APPLICANT: Ames, Robert S.
; APPLICANT: Appelbaum, Edward R.
; APPLICANT: Chaiken, Irwin M.
; APPLICANT: Cook, Richard M.
; APPLICANT: Gross, Mitchell S.
; APPLICANT: Holmes, Stephen D.
; APPLICANT: McMillan, Lynette J.
; APPLICANT: Theisen, Timothy W.
; TITLE OF INVENTION: Recombinant IL5 Antagonists Useful in
; TREATMENT OF IL5 Mediated Disorders
; NUMBER OF SEQUENCES: 74
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: SmithKline Beecham Corp./Corporate
; ADDRESSEE: Intellectual Property
; STREET: P. O. Box 1539-UW2220
; CITY: King of Prussia
; STATE: Pennsylvania
; COUNTRY: USA
; ZIP: 19406-0939
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/470,110A
; FILING DATE:
; CLASSIFICATION: 426
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/363131
; FILING DATE: 23-DEC-1994
; ATTORNEY/AGENT INFORMATION:
; NAME: Sutton, Jeffrey A.
; REGISTRATION NUMBER: 34,028
; REFERENCE/DOCKET NUMBER: P50282
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 610 270-5024
; TELEFAX: 610 270-5090
; INFORMATION FOR SEQ ID NO: 45:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 113 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-470-110A-45
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Best Local Similarity 91.2%; Pred. No. 2.2e-42;
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QY 64 DSGVPDRFTGSGSGDTFLITISSVQAE DLAVYYCNDHIYPYTFGGGKLEIK 116
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RESULT 3
US-08-667-769A-45
; Sequence 45, Application US/08667769A
; Patent No. 5783184
; GENERAL INFORMATION:
; APPLICANT: Ames, Robert S.
; APPLICANT: Appelbaum, Edward R.
; APPLICANT: Chaiken, Irwin M.
; APPLICANT: Cook, Richard M.
; APPLICANT: Gross, Mitchell S.
; APPLICANT: Holmes, Stephen D.
; APPLICANT: McMillan, Lynette J.
; APPLICANT: Theisen, Timothy W.
; TITLE OF INVENTION: Recombinant IL5 Antagonists Useful in
; TREATMENT OF IL5 Mediated Disorders
; NUMBER OF SEQUENCES: 76
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: SmithKline Beecham Corp./Corporate
; ADDRESSEE: P.O. Box 1539-UW2220
; CITY: King of Prussia
; STATE: Pennsylvania
; COUNTRY: USA
; ZIP: 19406-0939
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.30
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; APPLICATION NUMBER: US/08/667,769A
; FILING DATE:
; CLASSIFICATION: 424
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: PCT/US95/17082
; FILING DATE: 22-DEC-1995
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/470110
; FILING DATE: 06-JUN-1995
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/467420
; FILING DATE: 06-JUN-1995
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/363131
; FILING DATE: 23-DEC-1994
; ATTORNEY/AGENT INFORMATION:
; NAME: Sutton, Jeffrey A.
; REGISTRATION NUMBER: 34,028
; REFERENCE/DOCKET NUMBER: P50503
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 610-270-5024
; TELEFAX: 610-270-5090
; INFORMATION FOR SEQ ID NO: 45:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 113 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-667-769A-45
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QY 64 DSGVPDRFTGSGSGDTFLITISSVQAE DLAVYYCNDHIYPYTFGGGKLEIK 116
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Query Match	89.3%;	Score 541;	DB 2;	Length 113;
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; Appelbaum, Edward R.
; Chaiken, Irwin M.
; Cook, Richard M.
; Gross, Mitchell S.
; Holmes, Stephen D.
; McMillan, Lynette J.
; Theisen, Timothy W.
; TITLE OF INVENTION: Recombinant IL5 Antagonists Useful in
; Treatment of IL5 Mediated Disorders
; NUMBER OF SEQUENCES: 76
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: SmithKline Beecham Corp
; STREET: P.O. Box 1539-UW2220
; CITY: King of Prussia
; STATE: Pennsylvania
; COUNTRY: USA
; ZIP: 19406-0939
; COMPUTER READABLE FORM:
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; FILING DATE: 04-No. 6946130-2003
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/10/144,644
; FILING DATE: 2002-08-08
; APPLICATION NUMBER: US 08/470110
; FILING DATE: 06-JUN-1995
; APPLICATION NUMBER: US 08/467420
; FILING DATE: 08-JUN-1995
; APPLICATION NUMBER: US 08/363131
; FILING DATE: 23-DEC-1994
; ATTORNEY/AGENT INFORMATION:
; NAME: Sutton, Jeffrey A.
; REGISTRATION NUMBER: 34,028
; REFERENCE/DOCKET NUMBER: P50282-2
; TELEPHONE: 610-270-5024
; TELEFAX: 610-270-5090
; INFORMATION FOR SEQ ID NO: 45:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 113 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; SEQUENCE DESCRIPTION: SEQ ID NO: 45:

US-10-700-740-45

Query Match 89.3%; Score 541; DB 2; Length 113;
Best Local Similarity 91.2%; Pred. No. 2.2e-42;
Matches 103; Conservative 4; Mismatches 6; Indels 0; Gaps 0;

Qy 4 DIVMTQSPSSLSVSAAGEKVTMSCKSSQSLNSRQKNYLAWYQKPGQPPKLLIYGVR 63
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; Sequence 45, Application PC/TUS9517082A
; GENERAL INFORMATION:
; APPLICANT: Ames, Robert S.
; APPLICANT: Appelbaum, Edward R.
; APPLICANT: Chaiken, Irwin M.
; APPLICANT: Cook, Richard M.

; APPLICANT: Gross, Mitchell S.
; APPLICANT: Holmes, Stephen D.
; APPLICANT: McMillan, Lynette J.
; APPLICANT: Theisen, Timothy W.
; TITLE OF INVENTION: Recombinant IL5 Antagonists Useful in
; Treatment of IL5 Mediated Disorders
; NUMBER OF SEQUENCES: 76
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: SmithKline Beecham Corp./Corporate
; STREET: P.O. Box 1539-UW2220
; CITY: King of Prussia
; STATE: Pennsylvania
; COUNTRY: USA
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; APPLICATION NUMBER: US 08/470110
; FILING DATE: 06-JUN-1995
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/467420
; FILING DATE: 06-JUN-1995
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/363131
; FILING DATE: 23-DEC-1994
; ATTORNEY/AGENT INFORMATION:
; NAME: Sutton, Jeffrey A.
; REGISTRATION NUMBER: 34,028
; REFERENCE/DOCKET NUMBER: P50282-2
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 610-270-5024
; TELEFAX: 610-270-5090
; INFORMATION FOR SEQ ID NO: 45:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 113 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; PCT-US95-17082A-45

Query Match 89.3%; Score 541; DB 5; Length 113;
Best Local Similarity 91.2%; Pred. No. 2.2e-42;
Matches 103; Conservative 4; Mismatches 6; Indels 0; Gaps 0;

Qy 4 DIVMTQSPSSLSVSAAGEKVTMSCKSSQSLNSRQKNYLAWYQKPGQPPKLLIYGVR 63
Db 1 ELVMTQSPSSLSVSAAGEKVTMSCKSSQSLNSRQKNYLAWYQKPGQPPKLLIYGASTR 60

Qy 64 DSGVPDRFTGSGGTDFTLTITSSVQAEADLAVYYCONDHIYPVTFGGKLEIK 116
Db 61 ESGVPDRFTGSGGTDFTLTITSSVQAEADLAVYYCONDHSYPTFGSGKLEIK 113

RESULT 8
US-08-077-252B-4
; Sequence 4, Application US/08077252B
; Patent No. 5747654
; GENERAL INFORMATION:
; APPLICANT: Pastan, Ira
; APPLICANT: Lee, Byungkook
; APPLICANT: Jung, Sun-Hee
; APPLICANT: Brinkmann, Ulrich
; TITLE OF INVENTION: Recombinant Dieulfide-Stabilized
; Polypeptide Fragments Having Binding Specificity
; NUMBER OF SEQUENCES: 23

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; LOCATION: 93
; OTHER INFORMATION: /note= "V-I93 Ser to Tyr mutation site
; OTHER INFORMATION: (pseudo-symmetrically related to V-H97
; OTHER INFORMATION: Ser to Tyr mutation site in Heavy
; OTHER INFORMATION: chain variable region)"
; FEATURE:
; NAME/KEY: Region
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; OTHER INFORMATION: /label= CDR3
; OTHER INFORMATION: /note= "Complementarity Determining
; OTHER INFORMATION: Region 3 (CDR3)"
; FEATURE:
; NAME/KEY: Region
; LOCATION: 104..109
; OTHER INFORMATION: /label= FR4
; OTHER INFORMATION: /note= "Framework Region 4 (FR4)"
; FEATURE:
; NAME/KEY: Modified-site
; LOCATION: 106
; OTHER INFORMATION: /note= "Light chain variable region Ala
; OTHER INFORMATION: residue that can be changed to Cys,
; OTHER INFORMATION: paired with Heavy chain variable region
; OTHER INFORMATION: position 144 Arg residue change to Cys,
; OTHER INFORMATION: for possible SI site interchain
; OTHER INFORMATION: disulfide bond"
; US-08-077-252B-4
; Query Match 88.4%; Score 536; DB 1; Length 113;
; Best Local Similarity 91.2%; Pred. No. 6.3e-42;
; Matches 103; Conservative 3; Mismatches 7; Indels 0; Gaps
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DB 1 DIVMTQSPSSLSVSAGERVTWCKSKSSQLLNSGNQKNFLAWYQQKPGOPPKLLIYGASTR 60
QY 64 DSGVPRDTGSGSGTDFLTITSSVQAEDLAVYYCONDHIVPTFTGGTKLEIK 116
DB 61 ESGVPRDTGSGSGTDFLTITSSVQAEDLAVYYCONDHSYPLTFAGTKLEIK 113

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; REFERENCE/DOCKET NUMBER: 0610.1000001/MAC
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 202/371-2500
; TELEFAX: 202/371-2540
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 113 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-107-669D-2

Query Match      88.4%; Score 536; DB 1; Length 113;
Best Local Similarity 91.2%; Pred. No. 6.3e-42;
Matches 103; Conservative 3; Mismatches 7; Indels 0; Gaps 0;

QY 4 DIVMTQSPSSLSVSAGEKVTMTSCSKSSQSLNRSNQKNYLAWYQKPGQPPKLLIYGVFIR 63
Db 1 DIVMTQSPSSLSVSAGEKVTMTSCSKSSQSLNRSNQKNYLAWYQKPGQPPKLLIYGASTR 60

QY 64 DSGVPDRFTGSGGTDFTLTITSSVQAEADLAVYYCONDHIYPYTFGGGKLEIK 116
Db 61 ESGVPDRFTGSGGTDFTLTITSSVQAEADLAVYYCONDHSYPLTFGAGTKLEIK 113

RESULT 10
US-08-472-788A-2
; Sequence 2, Application US/08472788A
; Patent No. 5770196
; GENERAL INFORMATION:
; APPLICANT: Studnicka, Gary M.
; TITLE OF INVENTION: Modified Antibody Variable Domains
; NUMBER OF SEQUENCES: 89
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Sterne, Kessler, Goldstein and Fox P.L.L.C.
; STREET: 1100 New York Ave., N.W., Suite 600
; CITY: Washington
; STATE: D.C.
; COUNTRY: USA
; ZIP: 20005-3934
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/472,788A
; FILING DATE: 07-JUN-1995
; CLASSIFICATION: 424
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/082,842
; FILING DATE: 23-JUN-1993
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: PCT/US92/10906
; FILING DATE: 14-DEC-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/808,464
; FILING DATE: 13-DEC-1991
; ATTORNEY/AGENT INFORMATION:
; NAME: Cimbala, Michele A.
; REGISTRATION NUMBER: 33,851
; REFERENCE/DOCKET NUMBER: 0610.1000003
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 202/371-2500
; TELEFAX: 202/371-2540
; TELEX:
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 113 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-472-788A-2

; REFERENCE/DOCKET NUMBER: 0610.1000001/MAC
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 202/371-2500
; TELEFAX: 202/371-2540
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 113 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-107-669D-2

Query Match      88.4%; Score 536; DB 1; Length 113;
Best Local Similarity 91.2%; Pred. No. 6.3e-42;
Matches 103; Conservative 3; Mismatches 7; Indels 0; Gaps 0;

QY 4 DIVMTQSPSSLSVSAGEKVTMTSCSKSSQSLNRSNQKNYLAWYQKPGQPPKLLIYGVFIR 63
Db 1 DIVMTQSPSSLSVSAGEKVTMTSCSKSSQSLNRSNQKNYLAWYQKPGQPPKLLIYGASTR 60

QY 64 DSGVPDRFTGSGGTDFTLTITSSVQAEADLAVYYCONDHIYPYTFGGGKLEIK 116
Db 61 ESGVPDRFTGSGGTDFTLTITSSVQAEADLAVYYCONDHSYPLTFGAGTKLEIK 113

RESULT 11
US-08-477-531B-2
; Sequence 2, Application US/08477531B
; Patent No. 5821123
; GENERAL INFORMATION:
; APPLICANT: Studnicka, Gary M.
; TITLE OF INVENTION: Modified Antibody Variable Domains (as amended)
; NUMBER OF SEQUENCES: 67
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Sterne, Kessler, Goldstein and Fox P.L.L.C.
; STREET: 1100 New York Ave., N.W., Suite 600
; CITY: Washington
; STATE: D.C.
; COUNTRY: United States of America
; ZIP: 20005-3934
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/477,531B
; FILING DATE: 07-JUN-1995
; CLASSIFICATION: 436
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/107,669
; FILING DATE: 13-AUG-1993
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: PCT/US92/10906
; FILING DATE: 14-DEC-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/808,464
; FILING DATE: 13-DEC-1991
; ATTORNEY/AGENT INFORMATION:
; NAME: Michele A. Cimbala
; REGISTRATION NUMBER: 33,851
; REFERENCE/DOCKET NUMBER: 0610.1000004/MAC
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 202/371-2600
; TELEFAX: 202/371-2540
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 113 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-477-531B-2

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Best Local Similarity 91.2%; Pred. No. 6.3e-42;
Matches 103; Conservative 3; Mismatches 7; Indels 0; Gaps 0;

QY 4 DIVMTQSPSSLSVSAGEKVTMTSCSKSSQSLNRSNQKNYLAWYQKPGQPPKLLIYGVFIR 63
Db 1 DIVMTQSPSSLSVSAGEKVTMTSCSKSSQSLNRSNQKNYLAWYQKPGQPPKLLIYGASTR 60

QY 64 DSGVPDRFTGSGGTDFTLTITSSVQAEADLAVYYCONDHIYPYTFGGGKLEIK 116
Db 61 ESGVPDRFTGSGGTDFTLTITSSVQAEADLAVYYCONDHSYPLTFGAGTKLEIK 113
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RESULT 12

US-08-082-842A-2
; Sequence 2, Application US/08082842A
; Patent No. 585619
; GENERAL INFORMATION:
; APPLICANT: Studnicka, Gary M.
; TITLE OF INVENTION: Modified Antibody Variable Domains
; NUMBER OF SEQUENCES: 89
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Sterne, Kessler, Goldstein and Fox P.L.L.C.
; STREET: 1100 New York Ave., N.W., Suite 600
; CITY: Washington
; STATE: D.C.
; COUNTRY: USA
; ZIP: 20005-3934

COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/082,842A
; FILING DATE: 23-JUN-1993

CLASSIFICATION: 530
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: PCT/US92/10906
; FILING DATE: 14-DEC-1992

PRIOR APPLICATION DATA: US 07/808,464
; FILING DATE: 13-DEC-1991
; ATTORNEY/AGENT INFORMATION:
; NAME: Cimbala, Michele A.

REGISTRATION NUMBER: 33,851
; REFERENCE/DOCKET NUMBER: 0610.1000002
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 202/371-2600
; TELEFAX: 202/371-2540

TELEX:
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 113 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein

US-08-082-842A-2

Query Match 88.4%; Score 536; DB 1; Length 113;
Best Local Similarity 91.2%; Pred. No. 6.3e-42;
Matches 103; Conservative 3; Mismatches 7; Indels 0; Gaps 0;

QY 4 DIVMTQSPSSLSVAGEKVTMSCKSSQSLNSRNQKNYLAWYQKPGQPPKLLIYGVFIR 63

Db 1 DIVMTQSPSSLSVAGEKVTMSCKSSQSLNSRNQKNYLAWYQKPGQPPKLLIYGASTR 60

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Db 61 ESGVPRFTGSGSGDTFTLTISVQAEQLAVYYCQNDHSYPLTFGAGTGLEIK 113

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US-09-002-753A-4
; Sequence 4, Application US/09002753A
; Patent No. 6147203
; GENERAL INFORMATION:
; APPLICANT: Pastan, Ira

APPLICANT: Lee, Byungkook
; APPLICANT: Jung, Sun-Hee
; APPLICANT: Brinkmann, Ulrich

TITLE OF INVENTION: Recombinant Disulfide-Stabilized
; NUMBER OF SEQUENCES: 23

CORRESPONDENCE ADDRESS:
; ADDRESSEE: Townsend and Townsend and Crew LLP
; STREET: Two Embarcadero Center, Eighth Floor
; CITY: San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94111-3834
; COMPUTER READABLE FORM:
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; COMPUTER: IBM PC compatible
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; SOFTWARE: Patent In Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/002,753A
; FILING DATE: 05-JAN-1998
; CLASSIFICATION: 530
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/077,252
; FILING DATE: 14-JUN-1993
; ATTORNEY/AGENT INFORMATION:
; NAME: Weber, Ellen Lauver
; REGISTRATION NUMBER: 32,762
; REFERENCE/DOCKET NUMBER: 015280-152100US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 576-0200
; TELEFAX: (415) 576-0300
; INFORMATION FOR SEQ ID NO: 4:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 113 amino acids
; TYPE: amino acid
; STRANDEDNESS:
; TOPOLOGY: linear
; MOLECULE TYPE: protein
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; OTHER INFORMATION: Light chain variable region (V-L)"
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;   TOPOLOGY: linear
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;   LOCATION: 49
;   OTHER INFORMATION: /note= "Residue that can be changed"
;   OTHER INFORMATION: to Cys fro possible interchain disulfide bond."
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;   LOCATION: 63..94
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;   NAME/KEY: Modified-site
;   LOCATION: 106
;   OTHER INFORMATION: /note= "Residue that can be changed"
;   OTHER INFORMATION: to a Cys for possible interchain disulfide bond."
; FEATURE:
;   NAME/KEY: Modified-site
;   LOCATION: 93
;   OTHER INFORMATION: /note= "The Ser to Tyr mutation"
;   OTHER INFORMATION: site."
;
PCT-US94-06687-4

Query Match      88.4%; Score 536; DB 5; Length 113;
Best Local Similarity 91.2%; Pred. NO. 6.3e-42;
Matches 103; Conservative 3; Mismatches 7; Indels 0; Gaps 0;

QY 4 DIVMTQSPSSLSVAGEKVTMSCKSQSLNLRNKNKYLAWYQOKPGQPPKLLIYGVEIR 63
DB 1 DIVMTQSPSSLSVAGERVTMSCKSQSLNLRNKNKYLAWYQOKPGQPPKLLIYGASTR 60

QY 64 DSGVDPDRFTGSGSGDTFTLTISVQAEIDLAVYVQNDHIYPYTFGGGTGLEIK 116
DB 61 ESGVDPDRFTGSGSGDTFTLTISVQAEIDLAVYVQNDHSYPLTFGAGTGLEIK 113
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Search completed: May 19, 2006, 17:48:43

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GenCore version 5.1.8
Copyright (c) 1993 - 2006 Bioceleration Ltd.

OM protein - protein search, using sw model

Run on: May 19, 2006, 17:47:39 ; Search time 114.159 Seconds
(without alignments)
470.686 Million cell updates/sec

Title: US-09-889-936A-8

Perfect score: 606

Sequence: 1 SRGIVMTQSPSSLSVSAGE.....CONDHYPYTFGGTKLEIK 116

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 2097797 seqs, 463214858 residues

Total number of hits satisfying chosen parameters: 2097797

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Published Applications_AA_Main:*

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- 2: /EMC_Celerra_SIDS3/ptodata/2/pubpaa/US08_PUBCOMB.pep.*
- 3: /EMC_Celerra_SIDS3/ptodata/2/pubpaa/US09_PUBCOMB.pep.*
- 4: /EMC_Celerra_SIDS3/ptodata/2/pubpaa/US10A_PUBCOMB.pep.*
- 5: /EMC_Celerra_SIDS3/ptodata/2/pubpaa/US10B_PUBCOMB.pep.*
- 6: /EMC_Celerra_SIDS3/ptodata/2/pubpaa/US11_PUBCOMB.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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2	545	89.9	113	3	US-09-995-529-2	Sequence 2, Appl
3	541	89.3	113	4	US-10-144-644-45	Sequence 45, Appl
4	541	89.3	113	4	US-10-700-740-45	Sequence 45, Appl
5	541	89.3	113	6	US-11-076-395-45	Sequence 45, Appl
6	536	88.4	113	4	US-10-340-189-2	Sequence 2, Appl
7	536	88.4	113	4	US-10-325-696-2	Sequence 2, Appl
8	536	88.4	113	6	US-11-133-775-2	Sequence 2, Appl
9	536	88.4	115	5	US-10-700-632-68	Sequence 68, Appl
10	535	88.3	113	4	US-10-144-644-46	Sequence 46, Appl
11	535	88.3	113	4	US-10-700-740-46	Sequence 46, Appl
12	535	88.3	113	6	US-11-076-395-46	Sequence 46, Appl
13	526	86.8	113	4	US-10-144-644-16	Sequence 16, Appl
14	526	86.8	113	4	US-10-700-740-16	Sequence 16, Appl
15	526	86.8	113	6	US-11-076-395-16	Sequence 16, Appl
16	526	86.8	678	6	US-11-202-507A-11	Sequence 11, Appl
17	526	86.8	679	6	US-11-202-507A-5	Sequence 5, Appl
18	525	86.6	482	4	US-10-345-618-16	Sequence 16, Appl
19	523	86.3	118	5	US-10-491-653-148	Sequence 148, Appl
20	520	85.8	263	5	US-10-512-184-29	Sequence 29, Appl
21	518	85.5	115	3	US-09-998-831-9	Sequence 9, Appl
22	518	85.5	115	4	US-10-373-561-9	Sequence 9, Appl
23	518	85.5	115	5	US-10-738-404-9	Sequence 9, Appl
24	516	85.1	113	4	US-10-160-506-71	Sequence 71, Appl
25	516	85.1	113	4	US-10-160-506-91	Sequence 91, Appl
26	516	85.1	113	4	US-10-449-379-71	Sequence 71, Appl
27	516	85.1	113	4	US-10-449-379-91	Sequence 91, Appl

28	516	85.1	113	4	US-10-688-015-71	Sequence 71, Appl
29	516	85.1	113	4	US-10-688-015-91	Sequence 91, Appl
30	516	85.1	113	4	US-10-160-505-71	Sequence 71, Appl
31	516	85.1	113	4	US-10-160-505-91	Sequence 91, Appl
32	516	85.1	113	6	US-11-218-813-71	Sequence 71, Appl
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35	513	84.7	259	4	US-10-239-656-53	Sequence 53, Appl
36	513	84.7	378	5	US-10-743-697-1	Sequence 1, Appl
37	510	84.2	113	5	US-10-700-632-71	Sequence 71, Appl
38	510	84.2	258	4	US-10-239-656-71	Sequence 71, Appl
39	510	84.2	505	4	US-10-239-656-79	Sequence 79, Appl
40	507	83.7	255	4	US-10-239-656-69	Sequence 69, Appl
41	504	83.2	113	4	US-10-144-644-21	Sequence 21, Appl
42	504	83.2	113	4	US-10-700-740-21	Sequence 21, Appl
43	504	83.2	113	6	US-11-076-395-21	Sequence 21, Appl
44	495	81.7	115	5	US-10-700-632-64	Sequence 64, Appl
45	495	81.7	456	4	US-10-634-862-11	Sequence 11, Appl

ALIGNMENTS

RESULT 1

US-09-995-529-2
; Sequence 2, Application US/09995529
; Publication No. US2003009655A1
; GENERAL INFORMATION:
; APPLICANT: Watkins, Jeffrey D.
; APPLICANT: Huse, William D.
; APPLICANT: Tang, Ying
; TITLE OF INVENTION: Humanized Collagen Antibodies and
; FILE REFERENCE: P-IX 4976
; CURRENT APPLICATION NUMBER: US/09/995,529
; CURRENT FILING DATE: 2001-11-26
; NUMBER OF SEQ ID NOS: 358
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; ORGANISM: Mus musculus
US-09-995-529-2

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RESULT 2

US-09-995-529-2
; Sequence 2, Application US/09995529
; Publication No. US20040091482A9
; GENERAL INFORMATION:
; APPLICANT: Watkins, Jeffrey D.
; APPLICANT: Huse, William D.
; APPLICANT: Tang, Ying
; TITLE OF INVENTION: Humanized Collagen Antibodies and
; FILE REFERENCE: P-IX 4976
; CURRENT APPLICATION NUMBER: US/09/995,529
; CURRENT FILING DATE: 2001-11-26
; NUMBER OF SEQ ID NOS: 358
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 2

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; LENGTH: 113
; TYPE: PRT
; ORGANISM: Mus musculus
US-09-995-529-2

Query Match      89.9%; Score 545; DB 3; Length 113;
Best Local Similarity 92.9%; Pred. No. 2.9e-41;
Matches 105; Conservative 1; Mismatches 7; Indels 0; Gaps 0;

QY 4 DIVMTQSPSSLSVSAAGEKVTMSCKSSQSLNSRNQKNYLAWYQKPGPPKLLIYGVFIR 63
Db 1 DIVMTQSPSSLSVSAAGEKVTMSCKSSQSLNSRNQKNYLAWYQKPGPPKLLIYGASTR 60

QY 64 DSGVPDRFTGSGSGTDFLTITSSVQAEADLAVYYQNDHIYPTFTGGGKLEIK 116
Db 61 ESGVPDRFTGSGSGTDFLTITSSVQAEADLAVYYQNDHSDSYPTFTGGGKLEIK 113

RESULT 3
US-10-144-644-45
; Sequence 45, Application US/10144644
; Publication No. US20030059429A1
; GENERAL INFORMATION:
; APPLICANT: Ames, Robert S.
; APPLICANT: Appelbaum, Edward R.
; APPLICANT: Chaiken, Irwin M.
; APPLICANT: Cook, Richard M.
; APPLICANT: Gross, Mitchell S.
; APPLICANT: Holmes, Stephen D.
; APPLICANT: McMillan, Lynnette J.
; APPLICANT: Theisen, Timothy W.
; TITLE OF INVENTION: Recombinant IL5 Antagonists Useful in
; TITLE OF INVENTION: Treatment of IL5 Mediated Disorders
; NUMBER OF SEQUENCES: 76
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: SmithKline Beecham Corp
; STREET: P.O. Box 1539-UM2220
; CITY: King of Prussia
; STATE: Pennsylvania
; COUNTRY: USA
; ZIP: 19406-0939
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/10/144,644
; FILING DATE: 2002-08-08
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/470110
; FILING DATE: 06-JUN-1995
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/467420
; FILING DATE: 06-JUN-1995
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/363131
; FILING DATE: 23-DEC-1994
; ATTORNEY/AGENT INFORMATION:
; NAME: Sutton, Jeffrey A.
; REGISTRATION NUMBER: 34,028
; REFERENCE/DOCKET NUMBER: P50282-2
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 610-270-5024
; TELEFAX: 610-270-5090
; INFORMATION FOR SEQ ID NO: 45:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 113 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; SEQUENCE DESCRIPTION: SEQ ID NO: 45:

US-10-700-740-45
; Sequence 45, Application US/10700740
; Publication No. US20040156850A1
; GENERAL INFORMATION:
; APPLICANT: Ames, Robert S.
; APPLICANT: Appelbaum, Edward R.
; APPLICANT: Chaiken, Irwin M.
; APPLICANT: Cook, Richard M.
; APPLICANT: Gross, Mitchell S.
; APPLICANT: Holmes, Stephen D.
; APPLICANT: McMillan, Lynnette J.
; APPLICANT: Theisen, Timothy W.
; TITLE OF INVENTION: Recombinant IL5 Antagonists Useful in
; TITLE OF INVENTION: Treatment of IL5 Mediated Disorders
; NUMBER OF SEQUENCES: 76
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: SmithKline Beecham Corp
; STREET: P.O. Box 1539-UM2220
; CITY: King of Prussia
; STATE: Pennsylvania
; COUNTRY: USA
; ZIP: 19406-0939
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/10/700,740
; FILING DATE: 04-Nov-2003
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/10/144,644
; FILING DATE: 2002-08-08
; APPLICATION NUMBER: US 08/470110
; FILING DATE: 06-JUN-1995
; APPLICATION NUMBER: US 08/467420
; FILING DATE: 06-JUN-1995
; APPLICATION NUMBER: US 08/363131
; FILING DATE: 23-DEC-1994
; ATTORNEY/AGENT INFORMATION:
; NAME: Sutton, Jeffrey A.
; REGISTRATION NUMBER: 34,028
; REFERENCE/DOCKET NUMBER: P50282-2
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 610-270-5024
; TELEFAX: 610-270-5090
; INFORMATION FOR SEQ ID NO: 45:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 113 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; SEQUENCE DESCRIPTION: SEQ ID NO: 45:

US-10-700-740-45
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Query Match 89.3%; Score 541; DB 4; Length 113;
Best Local Similarity 91.2%; Pred. No. 6.6e-41;
Matches 103; Conservative 4; Mismatches 6; Indels 0; Gaps 0;

Qy 4 DIVWTQSPSSLSVAGKEVTMSCKSSQSLNSRNQKNYLAWYQKPGQPPKLLIYGAFIR 63
Db 1 ELVWTQSPSSLSVAGKEVTMSCKSSQSLNSRNQKNYLAWYQKPGQPPKLLIYGASTR 60
Qy 64 DSGVDPDRFTGSGSGTDFTLTISSVQAEADLAIVYQNDHIYPYTFGGGTGLEIK 116
Db 61 ESGVDPDRFTGSGSGTDFTLTISSVQAEADLAIVYQNDHSYPTFGSGTGLEIK 113

RESULT 5

US-11-076-395-45
; Sequence 45, Application US/11076395
; Publication No. US20060029594A1
; GENERAL INFORMATION:
; APPLICANT: Ames, Robert S.
; Appelbaum, Edward R.
; Chaiken, Irwin M.
; Cook, Richard M.
; Gross, Mitchell S.
; Holmes, Stephen D.
; McMillan, Lynette J.
; Thesen, Timothy W.
; TITLE OF INVENTION: Recombinant IL5 Antagonists Useful in
; Treatment of IL5 Mediated Disorders

NUMBER OF SEQUENCES: 76
CORRESPONDENCE ADDRESS:
ADDRESSEE: SmithKline Beecham Corp
STREET: P.O. Box 1539-UW2220
CITY: King of Prussia
STATE: Pennsylvania
COUNTRY: USA
ZIP: 19406-0939

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/11/076.395
FILING DATE: 09-Mar-2005
CLASSIFICATION: <Unknown>

PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/10/700,740
FILING DATE: 04-Nov-2003
APPLICATION NUMBER: US/10/144,644
FILING DATE: 2002-08-08
APPLICATION NUMBER: US 08/470110
FILING DATE: 06-JUN-1995
APPLICATION NUMBER: US 08/467420
FILING DATE: 06-JUN-1995
APPLICATION NUMBER: US 08/363131
FILING DATE: 23-DEC-1994

ATTORNEY/AGENT INFORMATION:
NAME: Sutton, Jeffrey A.
REGISTRATION NUMBER: 34,028
REFERENCE/DOCKET NUMBER: P50282-2
TELEPHONE: 610-270-5024
TELEFAX: 610-270-5090

INFORMATION FOR SEQ ID NO: 45:
SEQUENCE CHARACTERISTICS:
LENGTH: 113 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
SEQUENCE DESCRIPTION: SEQ ID NO: 45:

US-11-076-395-45

Query Match 89.3%; Score 541; DB 6; Length 113;
Best Local Similarity 91.2%; Pred. No. 6.6e-41;
Matches 103; Conservative 4; Mismatches 6; Indels 0; Gaps 0;

Qy 4 DIVWTQSPSSLSVAGKEVTMSCKSSQSLNSRNQKNYLAWYQKPGQPPKLLIYGAFIR 63
Db 1 ELVWTQSPSSLSVAGKEVTMSCKSSQSLNSRNQKNYLAWYQKPGQPPKLLIYGASTR 60
Qy 64 DSGVDPDRFTGSGSGTDFTLTISSVQAEADLAIVYQNDHIYPYTFGGGTGLEIK 116
Db 61 ESGVDPDRFTGSGSGTDFTLTISSVQAEADLAIVYQNDHSYPTFGSGTGLEIK 113

RESULT 6

US-10-340-189-2
; Sequence 2, Application US/10340189
; Publication No. US20030229207A1
; GENERAL INFORMATION:
; APPLICANT: Studnicka, Gary M.
; TITLE OF INVENTION: Modified Antibody Variable Domains
; NUMBER OF SEQUENCES: 89
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: McAndrews, Held & Malloy, Ltd.
; STREET: 500 W. Madison Street, 34th Floor
; CITY: Chicago
; STATE: Illinois
; COUNTRY: USA
; ZIP: 60661

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/340,189
FILING DATE: 10-Jan-2003
CLASSIFICATION: 530

PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/09/245,202A
FILING DATE: <Unknown>
APPLICATION NUMBER: 08/082,842
FILING DATE: 23-JUN-1993
APPLICATION NUMBER: PCT/US92/10906
FILING DATE: 14-DEC-1992
APPLICATION NUMBER: US 07/808,464
FILING DATE: 13-DEC-1991

ATTORNEY/AGENT INFORMATION:
NAME: McNicholas, Janet M.
REGISTRATION NUMBER: 32,918
REFERENCE/DOCKET NUMBER: 11023US07 / 200-71.P2.C2
TELEPHONE: 312/707-8889
TELEFAX: 312/707-9155
TELEX: <Unknown>

INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 113 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
SEQUENCE DESCRIPTION: SEQ ID NO: 2:

US-10-340-189-2

Query Match 88.4%; Score 536; DB 4; Length 113;
Best Local Similarity 91.2%; Pred. No. 1.9e-40;
Matches 103; Conservative 3; Mismatches 7; Indels 0; Gaps 0;

Qy 4 DIVWTQSPSSLSVAGKEVTMSCKSSQSLNSRNQKNYLAWYQKPGQPPKLLIYGAFIR 63
Db 1 DIVWTQSPSSLSVAGKEVTMSCKSSQSLNSRNQKNYLAWYQKPGQPPKLLIYGASTR 60
Qy 64 DSGVDPDRFTGSGSGTDFTLTISSVQAEADLAIVYQNDHIYPYTFGGGTGLEIK 116

Db 61 ESGVDPRTGSGSDFTLTISVQAEADLAVVYQNDHYSYPLTFGAGTKLEIK 113

RESULT 7

US-10-325-696-2

; Sequence 2, Application US/10325696

; Publication No. US20040005630A1

; GENERAL INFORMATION:

; APPLICANT: Studnicka, Gary M.

; TITLE OF INVENTION: Modified Antibody Variable Domains

; NUMBER OF SEQUENCES: 67

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: McAndrews, Held & Malloy, Ltd.

; STREET: 500 West Madison Street, 34th Floor

; CITY: Chicago

; STATE: IL

; COUNTRY: United States of America

; ZIP: 60661

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Floppy disk

; COMPUTER: IBM PC compatible

; OPERATING SYSTEM: PC-DOS/MS-DOS

; SOFTWARE: PatentIn Release #1.0, Version #1.25

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/10/325.696

; FILING DATE: 18-DEC-2002

; CLASSIFICATION: <Unknown>

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: US/09/097,980

; FILING DATE: 16-JUN-1998

; APPLICATION NUMBER: 08/107,669

; FILING DATE: 13-AUG-1993

; APPLICATION NUMBER: PCT/US92/10906

; FILING DATE: 14-DEC-1992

; ATTORNEY/AGENT INFORMATION:

; NAME: Janet M. McNicholas, Ph.D.

; REGISTRATION NUMBER: 32,918

; REFERENCE/DOCKET NUMBER: 11023US06/200-71.P1.C3

; TELECOMMUNICATION INFORMATION:

; TELEPHONE: 312/707-8889

; TELEFAX: 312/707-9050

; INFORMATION FOR SEQ ID NO: 2:

; SEQUENCE CHARACTERISTICS:

; LENGTH: 113 amino acids

; TYPE: amino acid

; TOPOLOGY: linear

; MOLECULE TYPE: protein

; SEQUENCE DESCRIPTION: SEQ ID NO: 2:

US-10-325-696-2

Query Match 88.4%; Score 536; DB 4; Length 113;

Best Local Similarity 91.2%; Pred. No. 1.9e-40;

Matches 103; Conservative 3; Mismatches 7; Indels 0; Gaps 0;

QY 4 DIVMTQSPSSLSVSAAGEKVTMSCKSSQSLNSRNQKNYLAWYQKPGQPPKLLIYGAFIR 63

Db 1 DIVMTQSPSSLSVSAGERVTMSCKSSQSLNSGNQKNFLAWYQKPGQPPKLLIYGASTR 60

QY 64 DSGVDPRTGSGSDFTLTISVQAEADLAVVYQNDHYSYPLTFGAGTKLEIK 116

Db 61 ESGVDPRTGSGSDFTLTISVQAEADLAVVYQNDHYSYPLTFGAGTKLEIK 113

RESULT 8

US-11-133-775-2

; Sequence 2, Application US/11133775

; Publication No. US20050239141A1

; GENERAL INFORMATION:

; APPLICANT: Studnicka, Gary M.

; TITLE OF INVENTION: Modified Antibody Variable Domains

; NUMBER OF SEQUENCES: 67

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: McAndrews, Held & Malloy, Ltd.

; STREET: 500 West Madison Street, 34th Floor

; CITY: Chicago

; STATE: IL

; COUNTRY: United States of America

; ZIP: 60661

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Floppy disk

; COMPUTER: IBM PC compatible

; OPERATING SYSTEM: PC-DOS/MS-DOS

; SOFTWARE: PatentIn Release #1.0, Version #1.25

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/11/133,775

; FILING DATE: 19-MAY-2005

; CLASSIFICATION:

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: US/09/097,980

; FILING DATE: 16-JUN-1998

; CLASSIFICATION:

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: 08/107,669

; FILING DATE: 13-AUG-1993

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: PCT/US92/10906

; FILING DATE: 14-DEC-1992

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: US 07/808,464

; FILING DATE: 13-DEC-1991

; ATTORNEY/AGENT INFORMATION:

; NAME: Janet M. McNicholas, Ph.D.

; REGISTRATION NUMBER: 32,918

; REFERENCE/DOCKET NUMBER: 11023US06/200-71.P1.C3

; TELECOMMUNICATION INFORMATION:

; TELEPHONE: 312/707-8889

; TELEFAX: 312/707-9050

; INFORMATION FOR SEQ ID NO: 2:

; SEQUENCE CHARACTERISTICS:

; LENGTH: 113 amino acids

; TYPE: amino acid

; TOPOLOGY: linear

; MOLECULE TYPE: protein

US-11-133-775-2

Query Match 88.4%; Score 536; DB 6; Length 113;

Best Local Similarity 91.2%; Pred. No. 1.9e-40;

Matches 103; Conservative 3; Mismatches 7; Indels 0; Gaps 0;

QY 4 DIVMTQSPSSLSVSAAGEKVTMSCKSSQSLNSRNQKNYLAWYQKPGQPPKLLIYGAFIR 63

Db 1 DIVMTQSPSSLSVSAGERVTMSCKSSQSLNSGNQKNFLAWYQKPGQPPKLLIYGASTR 60

QY 64 DSGVDPRTGSGSDFTLTISVQAEADLAVVYQNDHYSYPLTFGAGTKLEIK 116

Db 61 ESGVDPRTGSGSDFTLTISVQAEADLAVVYQNDHYSYPLTFGAGTKLEIK 113

RESULT 9

US-10-700-632-68

; Sequence 68, Application US/10700632

; Publication No. US20050118183A1

; GENERAL INFORMATION:

; APPLICANT: Immunogen, Inc.

; TITLE OF INVENTION: ANTI-CD33 ANTIBODIES AND METHODS FOR TREATMENT OF ACUTE MYELOID

; TITLE OF INVENTION: LEUKEMIA USING THE SAME

; FILE REFERENCE: A8427

; CURRENT APPLICATION NUMBER: US/10/700,632

; CURRENT FILING DATE: 2003-11-05

; PRIOR APPLICATION NUMBER: US 60/424,332

; PRIOR FILING DATE: 2002-11-07

; NUMBER OF SEQ ID NOS: 94

; SOFTWARE: PatentIn version 3.2

; SEQ ID NO 68

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US-10-144-644-46
Query Match      88.3%; Score 535; DB 4; Length 113;
Best Local Similarity 90.3%; Pred. NO. 2.3e-40;
Matches 102; Conservative 5; Mismatches 6; Indels 0; Gaps 0;

QY 4 DIVMTQSPSSLSVSAAGEKVTMSCKSSQSLNSRNQKNYLAWYQKPGPPKLLIYGAFIR 63
DB 1 ELVMTQSPSSLSVSAAGEKVTMSCKSSQSLNSGNQKNYLAWYQKPGPPKLLIYGASTR 60
QY 64 DSGVPRDRTGSGSGTDFLTITSSVQAEDLAVYYQNDSHIYPYTFGGGKLEIK 116
DB 61 ESGVPRDRTGSGSGTDFLTITSSVQAEDLAVYYQNDYSYPTFTSGTGKLEIK 113

RESULT 11
US-10-700-740-46
; Sequence 46, Application US/10700740
; Publication No. US20040156850A1
; GENERAL INFORMATION:
; APPLICANT: Ames, Robert S.
; Appelbaum, Edward R.
; Chaiken, Irwin M.
; Cook, Richard M.
; Gross, Mitchell S.
; Holmes, Stephen D.
; McMillan, Lynette J.
; Theisen, Timothy W.
; TITLE OF INVENTION: Recombinant IL5 Antagonists Useful in
; TREATMENT OF IL5 Mediated Disorders
; NUMBER OF SEQUENCES: 76
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: SmithKline Beecham Corp
; STREET: P.O. Box 1539-UW2220
; CITY: King of Prussia
; STATE: Pennsylvania
; COUNTRY: USA
; ZIP: 19406-0939
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/10/700.740
; FILING DATE: 04-Nov-2003
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/10/144.644
; FILING DATE: 2002-08-08
; APPLICATION NUMBER: US 08/470110
; FILING DATE: 06-JUN-1995
; APPLICATION NUMBER: US 08/467420
; FILING DATE: 06-JUN-1995
; APPLICATION NUMBER: US 08/363131
; FILING DATE: 23-DEC-1994
; ATTORNEY/AGENT INFORMATION:
; NAME: Sutton, Jeffrey A.
; REGISTRATION NUMBER: 34,028
; REFERENCE/DOCKET NUMBER: P50282-2
; TELEPHONE: 610-270-5024
; TELEFAX: 610-270-5090
; INFORMATION FOR SEQ ID NO: 46:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 113 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; SEQUENCE DESCRIPTION: SEQ ID NO: 46:
US-10-700-740-46

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Query Match 88.3%; Score 535; DB 4; Length 113;
Best Local Similarity 90.3%; Pred. No. 2.3e-40;
Matches 102; Conservative 5; Mismatches 6; Indels 0; Gaps 0;

QY 4 DIVMTQSPSSLSVSGAGEKVTMSCKSSQSLLNSRNQKNYLAWYQOKPGOPPKLLIYGVR 63
Db 1 ELVMTQSPSSLSVSGAGEKVTMSCKSSQSLLNSGNQKNYLAWYQOKPGOPPKLLIYGASTR 60

QY 64 DSGVDPDRFTGSGGTDFLTITSSVQAE DLAVYYCONDHLYPYTFGGGTKLEIK 116
Db 61 ESGVDPDRFTGSGGTDFLTITSSVQAE DLAVYYCONDYSYPTFGSGTKLEIK 113

RESULT 12
US-11-076-395-46
; Sequence 46, Application US/11076395
; Publication No. US20060029594A1
; GENERAL INFORMATION:
; APPLICANT: Ames, Robert S.
; Appelbaum, Edward R.
; Chaiken, Irwin M.
; Cook, Richard M.
; Gross, Mitchell S.
; Holmes, Stephen D.
; McMillan, Lynette J.
; Theisen, Timothy W.
; TITLE OF INVENTION: Recombinant IL5 Antagonists Useful in
; TREATMENT OF IL5 Mediated Disorders
; NUMBER OF SEQUENCES: 76
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: SmithKline Beecham Corp
; STREET: P.O. Box 1539-UM2220
; CITY: King of Prussia
; STATE: Pennsylvania
; COUNTRY: USA
; ZIP: 19406-0939
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/11/076,395
; FILING DATE: 09-Mar-2005
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/10/700,740
; FILING DATE: 04-Nov-2003
; APPLICATION NUMBER: US/10/144,644
; FILING DATE: 2002-08-08
; APPLICATION NUMBER: US 08/470110
; FILING DATE: 06-JUN-1995
; APPLICATION NUMBER: US 08/467420
; FILING DATE: 06-JUN-1995
; APPLICATION NUMBER: US 08/363131
; FILING DATE: 23-DEC-1994
; ATTORNEY/AGENT INFORMATION:
; NAME: Sutton, Jeffrey A.
; REGISTRATION NUMBER: 34,028
; REFERENCE/DOCKET NUMBER: P50282-2
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 610-270-5024
; TELEFAX: 610-270-5090
; INFORMATION FOR SEQ ID NO: 46:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 113 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; SEQUENCE DESCRIPTION: SEQ ID NO: 46:
US-11-076-395-46

Query Match 88.3%; Score 535; DB 6; Length 113;
Best Local Similarity 90.3%; Pred. No. 2.3e-40;
Matches 102; Conservative 5; Mismatches 6; Indels 0; Gaps 0;

QY 4 DIVMTQSPSSLSVSGAGEKVTMSCKSSQSLLNSRNQKNYLAWYQOKPGOPPKLLIYGVR 63
Db 1 ELVMTQSPSSLSVSGAGEKVTMSCKSSQSLLNSGNQKNYLAWYQOKPGOPPKLLIYGASTR 60

QY 64 DSGVDPDRFTGSGGTDFLTITSSVQAE DLAVYYCONDHLYPYTFGGGTKLEIK 116
Db 61 ESGVDPDRFTGSGGTDFLTITSSVQAE DLAVYYCONDYSYPTFGSGTKLEIK 113

RESULT 13
US-10-144-644-16
; Sequence 16, Application US/10144644
; Publication No. US20030059429A1
; GENERAL INFORMATION:
; APPLICANT: Ames, Robert S.
; APPLICANT: Appelbaum, Edward R.
; APPLICANT: Chaiken, Irwin M.
; APPLICANT: Cook, Richard M.
; APPLICANT: Gross, Mitchell S.
; APPLICANT: Holmes, Stephen D.
; APPLICANT: McMillan, Lynette J.
; APPLICANT: Theisen, Timothy W.
; TITLE OF INVENTION: Recombinant IL5 Antagonists Useful in
; TREATMENT OF IL5 Mediated Disorders
; NUMBER OF SEQUENCES: 76
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: SmithKline Beecham Corp
; STREET: P.O. Box 1539-UM2220
; CITY: King of Prussia
; STATE: Pennsylvania
; COUNTRY: USA
; ZIP: 19406-0939
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/10/144,644
; FILING DATE: 2002-08-08
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/470110
; FILING DATE: 06-JUN-1995
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/467420
; FILING DATE: 06-JUN-1995
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/363131
; FILING DATE: 23-DEC-1994
; ATTORNEY/AGENT INFORMATION:
; NAME: Sutton, Jeffrey A.
; REGISTRATION NUMBER: 34,028
; REFERENCE/DOCKET NUMBER: P50282-2
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 610-270-5024
; TELEFAX: 610-270-5090
; INFORMATION FOR SEQ ID NO: 16:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 113 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-10-144-644-16

Query Match 86.8%; Score 526; DB 4; Length 113;
Best Local Similarity 89.4%; Pred. No. 1.5e-39;
Matches 101; Conservative 5; Mismatches 7; Indels 0; Gaps 0;

Qy	4	DIWVTQSPSSLVSAGEKVTMSCKSSQSLNSRNQKYLAWYQQRPGQPKLLIIVGVFIR	63
Db ₂	1	DIWVTQSPSSLVSAGEKVTMSCKSSQSLNSRNQKYLAWYQQRPGQPKLLIIVGASTR	60
Qy	64	DSGVPRFRTGSGSGTFTLTIISSVQAEADLAVYYCNDHIYVPYTFGGGTLKLEIK	116
Db	61	ESGVPRFRTGSGSGTFTLTIISSVQAEADLAVYYCNVHFSPFTFGSGTLEIK	113

RESULT 14
US-10-700-740-16
; Sequence 16, Application US/10700740
; Publication No. US20040156850A1
; GENERAL INFORMATION:
; APPLICANT: Ames, Robert S.
; Appelbaum, Edward R.
; Chaiken, Irwin M.
; Cook, Richard M.
; Gross, Mitchell S.
; Holmes, Stephen D.
; McMillan, Lynette J.
; Theisen, Timothy W.
; TITLE OF INVENTION: Recombinant IL5 Antagonists Useful in
; Treatment of IL5 Mediated Disorders

Db	1	DIWVTQSPSSLSVSA	GKVT	MTSKSSQSLNSGNKQNYLAWYQOKPGQPKLLIYGASTR	60
Qy	64	DSGVPRFTGSGSGDT	FTLT	ISSVQAEELAVYYCQNDHIYPVTFGGGTGLEIK	116
Db	61	ESGVPRFTGSGSGDT	FTLT	ISSVQAEELAVYYCQNVHSPFTFGSGTGLEIK	113

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RESULT 15
US-11-076-395-16
; Sequence 16, Application US/11076395
; Publication No. US20060029594A1
; GENERAL INFORMATION:
; APPLICANT: Ames, Robert S.
; Appelbaum, Edward R.
; Chaiken, Irwin M.
; Cook, Richard M.
; Gross, Mitchell S.
; Holmes, Stephen D.
; McMillan, Lynette J.
; Theisen, Timothy W.
; TITLE OF INVENTION: Recombinant IL5 Antagonists Useful in
; IL5 Mediated Disorders
; NUMBER OF SEQUENCES: 76
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: SmithKline Beecham Corp
; STREET: P.O. Box 1539-UW220
; CITY: King of Prussia
; STATE: Pennsylvania
; COUNTRY: USA
; ZIP: 19406-0939
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/11/076,395
; FILING DATE: 09-Mar-2005
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/10/700,740
; FILING DATE: 04-Nov-2003
; APPLICATION NUMBER: US/10/144,644
; FILING DATE: 2002-08-08
; APPLICATION NUMBER: US 08/470110
; FILING DATE: 06-JUN-1995
; APPLICATION NUMBER: US 08/467420
; FILING DATE: 06-JUN-1995
; APPLICATION NUMBER: US 08/363131
; FILING DATE: 23-DEC-1994
; ATTORNEY/AGENT INFORMATION:
; NAME: Sutton, Jeffrey A.
; REGISTRATION NUMBER: 34,028
; REFERENCE/DOCKET NUMBER: P50282-2
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 610-270-5024
; TELEFAX: 610-270-5090
; INFORMATION FOR SEQ ID NO: 16:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 113 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; SEQUENCE DESCRIPTION: SEQ ID NO: 16:
US-11-076-395-16

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Db 1 DIVMTQSPSSLVSAGEKVTMSCKSSQSLNSGNQKNYLAWYQQKPGQPPKLLIYGASTR 60
Qy 64 DSGVPDRFTGSGSGTDFTLTISSVQAEDLAVYYCQNDHIYPYTFGGGTKLEIK 116
Db 61 ESGVPDRFTGSGSGTDFTLTISSVQAEDLAVYYCQNVHSFPFTFGSGTELEIK 113

Search completed: May 19, 2006, 17:52:58
Job time : 116.159 secs

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OM protein - protein search, using sw model

Run on: May 19, 2006, 17:49:02 ; Search time 5.52381 Seconds
(without alignments)
44.858 Million cell updates/sec

Title: US-09-889-936A-8
Perfect score: 606
Sequence: 1 SRGDIWQTSPSSLSVSAGE.....QNDHIHYPTFGGKLEIK 116

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 21570 seqs, 2136119 residues

Total number of hits satisfying chosen parameters: 21570

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Published Applications_AA New.*
1: /EMC_Celerra_SIDS3/ptodata/2/pubpaa/US09_NEW_PUB.pep.*
2: /EMC_Celerra_SIDS3/ptodata/2/pubpaa/US06_NEW_PUB.pep.*
3: /EMC_Celerra_SIDS3/ptodata/2/pubpaa/US07_NEW_PUB.pep.*
4: /EMC_Celerra_SIDS3/ptodata/2/pubpaa/US08_NEW_PUB.pep.*
5: /EMC_Celerra_SIDS3/ptodata/2/pubpaa/PCT_NEW_PUB.pep.*
6: /EMC_Celerra_SIDS3/ptodata/2/pubpaa/US10_NEW_PUB.pep.*
7: /EMC_Celerra_SIDS3/ptodata/2/pubpaa/US11_NEW_PUB.pep.*
8: /EMC_Celerra_SIDS3/ptodata/2/pubpaa/US60_NEW_PUB.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	536	88.4	118	7	US-11-075-891-26 Sequence 26, Appl
2	516	85.1	113	7	US-11-219-563-71 Sequence 71, Appl
3	516	85.1	113	7	US-11-219-563-91 Sequence 91, Appl
4	493	79.7	113	7	US-11-219-563-72 Sequence 72, Appl
5	470	77.6	115	7	US-11-219-563-92 Sequence 92, Appl
6	452.5	74.7	133	6	US-10-511-937-2965 Sequence 2965, Ap
7	442	72.9	115	7	US-11-254-679-5 Sequence 5, Appl
8	412	68.0	107	7	US-11-221-902-23 Sequence 23, Appl
9	412	68.0	214	7	US-11-221-902-11 Sequence 11, Appl
10	404	66.7	101	7	US-11-221-902-63 Sequence 63, Appl
11	404	66.7	101	7	US-11-239-308-57 Sequence 57, Appl
12	391	64.5	217	7	US-11-221-902-17 Sequence 17, Appl
13	391	64.5	214	7	US-11-221-902-5 Sequence 5, Appl
14	391	64.5	214	7	US-11-221-902-7 Sequence 7, Appl
15	391	64.5	214	7	US-11-221-902-9 Sequence 9, Appl
16	391	64.5	254	7	US-11-075-891-6 Sequence 6, Appl
17	391	64.5	254	7	US-11-075-891-8 Sequence 8, Appl
18	391	64.5	254	7	US-11-075-891-10 Sequence 10, Appl
19	390	64.4	107	7	US-11-254-182-1 Sequence 1, Appl
20	386	63.7	110	7	US-11-075-891-28 Sequence 28, Appl
21	385	63.5	107	7	US-11-219-563-64 Sequence 64, Appl
22	383	63.2	107	7	US-11-254-182-5 Sequence 5, Appl
23	383	63.2	108	7	US-11-254-182-27 Sequence 27, Appl
24	383	63.2	108	7	US-11-219-121-23 Sequence 23, Appl
25	383	63.2	108	7	US-11-106-762-19 Sequence 19, Appl

ALIGNMENTS

RESULT 1
US-11-075-891-26
; Sequence 26, Application US/11075891
; Publication No. US20060088521A1
; GENERAL INFORMATION:
; APPLICANT: MAHADEVAN, DARUKA
; TITLE OF INVENTION: COMPOSITION AND METHOD FOR CANCER TREATMENT
; FILE REFERENCE: 263922US96
; CURRENT APPLICATION NUMBER: US/11/075,891
; CURRENT FILING DATE: 2005-03-10
; PRIOR APPLICATION NUMBER: US 60/557,258
; PRIOR FILING DATE: 2004-03-27
; NUMBER OF SEQ ID NOS: 36
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 26
; LENGTH: 118
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetic Peptide
US-11-075-891-26

Query Match		88.4%;	Score 536;	DB 7;	Length 118;
Best Local Similarity		91.2%;	Pred. No. 8e-25;	7;	Indels 0;
Matches 103;		Conservative 3;	Mismatches 7;	Indels 0;	Gaps 0;
QY	4	DIWMTQSPSSLSVSAGEKVTMSCKSSQSLNSRNKNYLAWYQKPGQPPKLLIYGVFIR	63		
Db	1	DIWMTQSPSSLSVSAGERVTMSCKSSQSLNSGNKNFLAWYQKPGQPPKLLIYGASTR	60		
QY	64	DSGVPRDFTGSGSGTDFLTITISVQAEDLAVYQCNDHIHYPTFGGKLEIK	116		
Db	61	ESGVPRDFTGSGSGTDFLTITISVQAEDLAVYQCNDHSYPLTFGAGTKLEIK	113		
RESULT 2					
US-11-219-563-71					
; Sequence 71, Application US/11219563					
; Publication No. US20060088539A1					
; GENERAL INFORMATION:					
; APPLICANT: Bander, Neil					
; TITLE OF INVENTION: MODIFIED ANTIBODIES TO PROSTATE-SPECIFIC					
; TITLE OF INVENTION: MEMBRANE ANTIGEN AND USES THEREOF					
; FILE REFERENCE: 13651.001 (BZL-001)					
; CURRENT APPLICATION NUMBER: US/11/219,563					
; CURRENT FILING DATE: 2005-09-02					
; PRIOR APPLICATION NUMBER: PCT/US04/06586					
; PRIOR FILING DATE: 2004-03-03					

Sequence 27, Appl
Sequence 6, Appl1
Sequence 66, Appl
Sequence 12, Appl
Sequence 14, Appl
Sequence 16, Appl
Sequence 67, Appl
Sequence 31, Appl
Sequence 3, Appl1
Sequence 63, Appl
Sequence 4, Appl1
Sequence 15, Appl
Sequence 23, Appl
Sequence 17, Appl
Sequence 50, Appl
Sequence 65, Appl
Sequence 68, Appl
Sequence 48, Appl
Sequence 10, Appl
Sequence 21, Appl

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; PRIOR APPLICATION NUMBER: US 10/379,838
; PRIOR FILING DATE: 2003-03-03
; PRIOR APPLICATION NUMBER: 10/449,379
; PRIOR FILING DATE: 2003-05-30
; NUMBER OF SEQ ID NOS: 144
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 71
; LENGTH: 113
; TYPE: PRT
; ORGANISM: Mus musculus
US-11-219-563-71

Query Match      85.1%; Score 516; DB 7; Length 113;
Best Local Similarity 88.5%; Pred. No. 9.8e-24;
Matches 100; Conservative 4; Mismatches 9; Indels 0; Gaps 0;

QY 4 DIVMTQSPSSLSVSAAGEKVTMSCKSSQSLNLRNOKNYLAWYQKPGQPPKLLIYGVFIR 63
Db 1 DIVMTQSPSSLSVSAAGEKVTMSCKSSQSLNLRNOKNYLAWYQKPGQPPKLLIYWASTR 60

QY 64 DSGVPDRFTGSGGDTFTLTISVQAEDLAVYYCONDHIYPYTFGGGKLEIK 116
Db 61 ESGVPDRFTGSGGDTFTLTISVQAEDLAVYYCONDYSPYPLTFGAGTKLEIK 113

RESULT 3
US-11-219-563-91
; Sequence 91, Application US/11219563
; Publication No. US20060088539A1
; GENERAL INFORMATION:
; APPLICANT: Bander, Neil
; TITLE OF INVENTION: MODIFIED ANTIBODIES TO PROSTATE-SPECIFIC
; FILE REFERENCE: 13651.001 (BZL-001)
; CURRENT APPLICATION NUMBER: US/11/219,563
; CURRENT FILING DATE: 2005-09-02
; PRIOR APPLICATION NUMBER: PCT/US04/06586
; PRIOR FILING DATE: 2004-03-03
; PRIOR APPLICATION NUMBER: US 10/379,838
; PRIOR FILING DATE: 2003-03-03
; PRIOR APPLICATION NUMBER: 10/449,379
; PRIOR FILING DATE: 2003-05-30
; NUMBER OF SEQ ID NOS: 144
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 91
; LENGTH: 113
; TYPE: PRT
; ORGANISM: Mus musculus
US-11-219-563-91

Query Match      85.1%; Score 516; DB 7; Length 113;
Best Local Similarity 88.5%; Pred. No. 9.8e-24;
Matches 100; Conservative 4; Mismatches 9; Indels 0; Gaps 0;

QY 4 DIVMTQSPSSLSVSAAGEKVTMSCKSSQSLNLRNOKNYLAWYQKPGQPPKLLIYGVFIR 63
Db 1 DIVMTQSPSSLSVSAAGEKVTMSCKSSQSLNLRNOKNYLAWYQKPGQPPKLLIYWASTR 60

QY 64 DSGVPDRFTGSGGDTFTLTISVQAEDLAVYYCONDHIYPYTFGGGKLEIK 116
Db 61 ESGVPDRFTGSGGDTFTLTISVQAEDLAVYYCONDYSPYPLTFGAGTKLEIK 113

RESULT 4
US-11-219-563-72
; Sequence 72, Application US/11219563
; Publication No. US20060088539A1
; GENERAL INFORMATION:
; APPLICANT: Bander, Neil
; TITLE OF INVENTION: MODIFIED ANTIBODIES TO PROSTATE-SPECIFIC
; FILE REFERENCE: 13651.001 (BZL-001)
; CURRENT APPLICATION NUMBER: US/11/219,563
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; CURRENT FILING DATE: 2005-09-02
; PRIOR APPLICATION NUMBER: PCT/US04/06586
; PRIOR FILING DATE: 2004-03-03
; PRIOR APPLICATION NUMBER: US 10/379,838
; PRIOR FILING DATE: 2003-03-03
; PRIOR APPLICATION NUMBER: 10/449,379
; PRIOR FILING DATE: 2003-05-30
; NUMBER OF SEQ ID NOS: 144
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 72
; LENGTH: 113
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: majority sequence
US-11-219-563-72

Query Match      79.7%; Score 483; DB 7; Length 113;
Best Local Similarity 81.4%; Pred. No. 6.5e-22;
Matches 92; Conservative 9; Mismatches 12; Indels 0; Gaps 0;

QY 4 DIVMTQSPSSLSVSAAGEKVTMSCKSSQSLNLRNOKNYLAWYQKPGQPPKLLIYGVFIR 63
Db 1 DIVMTQSPSSLSVSAAGEKVTMSCKSSQSLNLRNOKNYLAWYQKPGQPPKLLIYGASTR 60

QY 64 DSGVPDRFTGSGGDTFTLTISVQAEDLAVYYCONDHIYPYTFGGGKLEIK 116
Db 61 ESGVPDRFTGSGGDTFTLTISVQAEDLAVYYCNSYSFPLTFGGGKLEIK 113

RESULT 5
US-11-219-563-92
; Sequence 92, Application US/11219563
; Publication No. US20060088539A1
; GENERAL INFORMATION:
; APPLICANT: Bander, Neil
; TITLE OF INVENTION: MODIFIED ANTIBODIES TO PROSTATE-SPECIFIC
; FILE REFERENCE: 13651.001 (BZL-001)
; CURRENT APPLICATION NUMBER: US/11/219,563
; CURRENT FILING DATE: 2005-09-02
; PRIOR APPLICATION NUMBER: PCT/US04/06586
; PRIOR FILING DATE: 2004-03-03
; PRIOR APPLICATION NUMBER: US 10/379,838
; PRIOR FILING DATE: 2003-03-03
; PRIOR APPLICATION NUMBER: 10/449,379
; PRIOR FILING DATE: 2003-05-30
; NUMBER OF SEQ ID NOS: 144
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 92
; LENGTH: 115
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: majority sequence
US-11-219-563-92

Query Match      77.6%; Score 470; DB 7; Length 115;
Best Local Similarity 79.6%; Pred. No. 3.4e-21;
Matches 90; Conservative 10; Mismatches 13; Indels 0; Gaps 0;

QY 4 DIVMTQSPSSLSVSAAGEKVTMSCKSSQSLNLRNOKNYLAWYQKPGQPPKLLIYGVFIR 63
Db 1 DIVMTQSPSSLSVSAAGEKVTMSCKSSQSLNLRNOKNYLAWYQKPGQPPKLLIYSASTR 60

QY 64 DSGVPDRFTGSGGDTFTLTISVQAEDLAVYYCONDHIYPYTFGGGKLEIK 116
Db 61 ESGVPDRFTGSGGDTFTLTISVQAEDLAVYFCQNDNSYPLTFGAGTKLEIK 113

RESULT 6
US-10-511-937-2965
; Sequence 2965, Application US/10511937
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; ORGANISM: Homo sapiens
US-11-254-679-5

Query Match          72.9%; Score 442; DB 7; Length 115;
Best Local Similarity 75.2%; Pred. No. 1.2e-19;
Matches      85; Conservative   11; Mismatches    17; Indels     0; Gaps     0;

Qy  4 DIVMTQPSLSVSAGKVTWMSCKSSQSLLNSRNKNYLAWYQQKPGPPKLLIYGVFIR 63
| | | | | | | | | | : | : | : | : | | | : | : | : | : | : | : | : |
Db  3 DIQMTPSDSLAVSLGERATINCKSSQSVLSSNNKNVLAWYQQKPGPPKLLIYWASTR 62
| | | | | | | | | | : | : | : | : | | | : | : | : | : | : | : | : |
Qy  64 DSGVPDRFTGSGGTDTFLTITSSVQAEDLAVYYCONDHIYPYTFGGGTKLEIK 116
| | | | | | | | | | : | : | : | : | : | : | : | : | : | : | : | : |
Db  63 ESGVPDRFSGSGGTDTFLTITSSVQAEDLAVYYCOQDYSTPRTFGGGTKVEIK 115
| | | | | | | | | | : | : | : | : | : | : | : | : | : | : | : | : |

RESULT 8
US-11-221-902-23
; Sequence 23, Application US/11221902
; Publication No. US2006008522A1
; GENERAL INFORMATION:
; APPLICANT: Wyeth
; TITLE OF INVENTION: HUMANIZED ANTI-5T4 ANTIBODIES AND ANTI-5T4/CALICHEAMICIN CONJUGATE
; FILE REFERENCE: 040000-0317285
; CURRENT APPLICATION NUMBER: US/11/221,902
; CURRENT FILING DATE: 2005-09-09
; NUMBER OF SEQ ID NOS: 89
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 23
; LENGTH: 107
; TYPE: PRT
; ORGANISM: Artificial
; FEATURE:
; OTHER INFORMATION: artificial sequence is derived from mouse and human antibody
; OTHER INFORMATION: sequences
US-11-221-902-23

Query Match          68.0%; Score 412; DB 7; Length 107;
Best Local Similarity 71.7%; Pred. No. 5.2e-18;
Matches      81; Conservative   12; Mismatches    14; Indels     6; Gaps     1;

Qy  4 DIVMTQPSLSVSAGKVTWMSCKSSQSLLNSRNKNYLAWYQQKPGPPKLLIYGVFIR 63
| | | | | | | | | | : | : | : | : | | | : | : | : | : | : | : | : |
Db  1 DIVMTQSPDSLAVSLGERATINCKASQSVSND-----VAWYQQKPGPPKLLIYTSSR 54
| | | | | | | | | | : | : | : | : | | | : | : | : | : | : | : | : |
Qy  64 DSGVPDRFTGSGGTDTFLTITSSVQAEDLAVYYCONDHIYPYTFGGGTKLEIK 116
| | | | | | | | | | : | : | : | : | : | : | : | : | : | : | : | : |
Db  55 YAGVPDRFSGSGGTDTFLTITSSVQAEDLAVYYCOQDYNSPPTFGGGTKLEIK 107
| | | | | | | | | | : | : | : | : | : | : | : | : | : | : | : | : |

RESULT 9
US-11-221-902-11
; Sequence 11, Application US/11221902
; Publication No. US2006008522A1
; GENERAL INFORMATION:
; APPLICANT: Wyeth
; TITLE OF INVENTION: HUMANIZED ANTI-5T4 ANTIBODIES AND ANTI-5T4/CALICHEAMICIN CONJUGATE
; FILE REFERENCE: 040000-0317285
; CURRENT APPLICATION NUMBER: US/11/221,902
; CURRENT FILING DATE: 2005-09-09
; NUMBER OF SEQ ID NOS: 89
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 11
; LENGTH: 214
; TYPE: PRT
; ORGANISM: Artificial
; FEATURE:
; OTHER INFORMATION: artificial sequence is derived from mouse and human antibody
; OTHER INFORMATION: sequences
; FEATURE:
; NAME/KEY: MISC_FEATURE
; LOCATION: (1)..(107)
; OTHER INFORMATION: light chain variable region
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; FEATURE:
; NAME/KEY: MISC FEATURE
; LOCATION: (24)..(34)
; OTHER INFORMATION: CDR 1
; FEATURE:
; NAME/KEY: MISC FEATURE
; LOCATION: (50)..(56)
; OTHER INFORMATION: CDR 2
; FEATURE:
; NAME/KEY: MISC FEATURE
; LOCATION: (89)..(97)
; OTHER INFORMATION: CDR3
US-11-221-902-11

Query Match      68.0%; Score 412; DB 7; Length 214;
Best Local Similarity 71.7%; Pred. No. 8.2e-18;
Matches 81; Conservative 12; Mismatches 14; Indels 6; Gaps 1;

QY 4 DIVMTQSPSSLSVSGAGEKVTMSCKSSQSLNSRNQKNYLAWYQOKPGOPPKLLIYGVFIR 63
Db 1 DIVMTQSPDSLAVSLGERATINCKASQSVND-----VAVYQKPGQPKLLIYTSR 54

QY 64 DSGVPDRFTGSGSGTDFTLTISSVQAEADLVAVYQNDHIYP 116
Db 55 YAGVDPDRFSGSGGTDFTLTISSLQAEADVAVYCCQDYNSTPTFGGKLEIK 107

RESULT 10
US-11-221-902-63
; Sequence 63, Application US/11221902
; Publication No. US20060088522A1
; GENERAL INFORMATION:
; APPLICANT: Wyeth
; TITLE OF INVENTION: HUMANIZED ANTI-5T4 ANTIBODIES AND ANTI-5T4/CALICHEAMICIN CONJUGATE
; FILE REFERENCE: 040000-0317285
; CURRENT APPLICATION NUMBER: US/11/221,902
; CURRENT FILING DATE: 2005-09-09
; NUMBER OF SEQ ID NOS: 89
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 63
; LENGTH: 101
; TYPE: PRT
; ORGANISM: Homo sapiens
US-11-221-902-63

Query Match      66.7%; Score 404; DB 7; Length 101;
Best Local Similarity 76.2%; Pred. No. 1.4e-17;
Matches 77; Conservative 10; Mismatches 14; Indels 0; Gaps 0;

QY 4 DIVMTQSPSSLSVSGAGEKVTMSCKSSQSLNSRNQKNYLAWYQOKPGOPPKLLIYGVFIR 63
Db 1 DIVMTQSPDSLAVSLGERATINCKSSQSVLYSSNNKYNLAWYQOKPGOPPKLLIYWASTR 60

QY 64 DSGVPDRFTGSGSGTDFTLTISSVQAEADLVAVYQNDHIYP 104
Db 61 ESGVDPDRFSGSGGTDFTLTISSLQAEADVAVYCCQYVSTP 101

RESULT 11
US-11-239-308-57
; Sequence 57, Application US/11239308
; Publication No. US2006008883A1
; GENERAL INFORMATION:
; APPLICANT: Smider, Vaughn
; APPLICANT: Larrick, James W.
; APPLICANT: Integrigen, Inc.
; TITLE OF INVENTION: Recombinant Catalytic Polypeptides and Their Uses
; FILE REFERENCE: 021216-000310US
; CURRENT APPLICATION NUMBER: US/11/239,308
; CURRENT FILING DATE: 2003-09-28
; PRIOR APPLICATION NUMBER: US/10/683,733
; PRIOR FILING DATE: 2003-10-09
; PRIOR APPLICATION NUMBER: US 60/417,979
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; PRIOR FILING DATE: 2002-10-09
; NUMBER OF SEQ ID NOS: 62
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 57
; LENGTH: 101
; TYPE: PRT
; ORGANISM: Homo sapiens
US-11-239-308-57

Query Match      66.7%; Score 404; DB 7; Length 101;
Best Local Similarity 76.2%; Pred. No. 1.4e-17;
Matches 77; Conservative 10; Mismatches 14; Indels 0; Gaps 0;

QY 4 DIVMTQSPSSLSVSGAGEKVTMSCKSSQSLNSRNQKNYLAWYQOKPGOPPKLLIYGVFIR 63
Db 1 DIVMTQSPDSLAVSLGERATINCKSSQSVLYSSNNKYNLAWYQOKPGOPPKLLIYWASTR 60

QY 64 DSGVPDRFTGSGSGTDFTLTISSVQAEADLVAVYQNDHIYP 104
Db 61 ESGVDPDRFSGSGGTDFTLTISSLQAEADVAVYCCQYVSTP 101

RESULT 12
US-11-221-902-17
; Sequence 17, Application US/11221902
; Publication No. US20060088522A1
; GENERAL INFORMATION:
; APPLICANT: Wyeth
; TITLE OF INVENTION: HUMANIZED ANTI-5T4 ANTIBODIES AND ANTI-5T4/CALICHEAMICIN CONJUGATE
; FILE REFERENCE: 040000-0317285
; CURRENT APPLICATION NUMBER: US/11/221,902
; CURRENT FILING DATE: 2005-09-09
; NUMBER OF SEQ ID NOS: 89
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 17
; LENGTH: 107
; TYPE: PRT
; ORGANISM: Artificial
; FEATURE:
; OTHER INFORMATION: artificial sequence is derived from mouse and human antibody
; OTHER INFORMATION: sequence
US-11-221-902-17

Query Match      64.5%; Score 391; DB 7; Length 107;
Best Local Similarity 69.0%; Pred. No. 7.4e-17;
Matches 78; Conservative 13; Mismatches 16; Indels 6; Gaps 1;

QY 4 DIVMTQSPSSLSVSGAGEKVTMSCKSSQSLNSRNQKNYLAWYQOKPGOPPKLLIYGVFIR 63
Db 1 DIVMTQSPDSLAVSLGERATINCKASQSVND-----VAVYQKPGQPKLLIYTSR 54

QY 64 DSGVPDRFTGSGSGTDFTLTISSVQAEADLVAVYQNDHIYP 116
Db 55 YAGVDPDRFSGSGGTDFTLTISSLQAEADVAVYCCQDYNSTPTFGGKLEIK 107

RESULT 13
US-11-221-902-5
; Sequence 5, Application US/11221902
; Publication No. US20060088522A1
; GENERAL INFORMATION:
; APPLICANT: Wyeth
; TITLE OF INVENTION: HUMANIZED ANTI-5T4 ANTIBODIES AND ANTI-5T4/CALICHEAMICIN CONJUGATE
; FILE REFERENCE: 040000-0317285
; CURRENT APPLICATION NUMBER: US/11/221,902
; CURRENT FILING DATE: 2005-09-09
; NUMBER OF SEQ ID NOS: 89
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 5
; LENGTH: 214
; TYPE: PRT
; ORGANISM: Artificial
; FEATURE:
```

OTHER INFORMATION: artificial sequence is derived from mouse and human antibody
FEATURE:
NAME/KEY: MISC_FEATURE
LOCATION: (1)..(107)
OTHER INFORMATION: light chain variable region
US-11-221-902-5

Query Match 64.5%; Score 391; DB 7; Length 214;
Best Local Similarity 69.0%; Pred. No. 1.2e-16;
Matches 78; Conservative 13; Mismatches 16; Indels 6; Gaps 1;
QY 4 DIVMTQSPSSLSVAGEKVTMSCKSSQSLNRSNKNYLAWYQOKPGQPPKLLIYGVFIR 63
Db 1 DIVMTQSPDSLAVSLGERATINCKASQSVND-----VAVYQKPGQSPKLLISYTSR 54
QY 64 DSGVPDRFTGSGSGTDTLTITSSVQAEADLAVYVCQNDHIYPYTFGGGTTKLEIK 116
Db 55 YAGVDPDRFSGSGSGTDTLTITSSVQAEADLAVYFCQDYNPSPTFGGTTKLEIK 107

RESULT 14
US-11-221-902-7
Sequence 7, Application US/11221902
Publication No. US20060088522A1
GENERAL INFORMATION:
APPLICANT: Wyeth
TITLE OF INVENTION: HUMANIZED ANTI-5T4 ANTIBODIES AND ANTI-5T4/CALICHEAMICIN CONJUGAT
FILE REFERENCE: 040000-0317285
CURRENT APPLICATION NUMBER: US/11/221,902
CURRENT FILING DATE: 2005-09-09
NUMBER OF SEQ ID NOS: 89
SOFTWARE: PatentIn version 3.3
SEQ ID NO 7
LENGTH: 214
TYPE: PRT
ORGANISM: Artificial
FEATURE:
OTHER INFORMATION: artificial sequence is derived from mouse and human antibody
OTHER INFORMATION: sequences
FEATURE:
NAME/KEY: MISC_FEATURE
LOCATION: (1)..(107)
OTHER INFORMATION: light chain variable region
US-11-221-902-7

Query Match 64.5%; Score 391; DB 7; Length 214;
Best Local Similarity 69.0%; Pred. No. 1.2e-16;
Matches 78; Conservative 13; Mismatches 16; Indels 6; Gaps 1;
QY 4 DIVMTQSPSSLSVAGEKVTMSCKSSQSLNRSNKNYLAWYQOKPGQPPKLLIYGVFIR 63
Db 1 DIVMTQSPDSLAVSLGERATINCKASQSVND-----VAVYQKPGQSPKLLISYTSR 54
QY 64 DSGVPDRFTGSGSGTDTLTITSSVQAEADLAVYVCQNDHIYPYTFGGGTTKLEIK 116
Db 55 YAGVDPDRFSGSGSGTDTLTITSSVQAEADLAVYFCQDYNPSPTFGGTTKLEIK 107

RESULT 15
US-11-221-902-9
Sequence 9, Application US/11221902
Publication No. US20060088522A1
GENERAL INFORMATION:
APPLICANT: Wyeth
TITLE OF INVENTION: HUMANIZED ANTI-5T4 ANTIBODIES AND ANTI-5T4/CALICHEAMICIN CONJUGAT
FILE REFERENCE: 040000-0317285
CURRENT APPLICATION NUMBER: US/11/221,902
CURRENT FILING DATE: 2005-09-09
NUMBER OF SEQ ID NOS: 89
SOFTWARE: PatentIn version 3.3
SEQ ID NO 9
LENGTH: 214

TYPE: PRT
ORGANISM: Artificial
FEATURE:
OTHER INFORMATION: artificial sequence is derived from mouse and human antibody
OTHER INFORMATION: sequences
FEATURE:
NAME/KEY: MISC_FEATURE
LOCATION: (1)..(107)
OTHER INFORMATION: light chain variable region
US-11-221-902-9
Query Match 64.5%; Score 391; DB 7; Length 214;
Best Local Similarity 69.0%; Pred. No. 1.2e-16;
Matches 78; Conservative 13; Mismatches 16; Indels 6; Gaps 1;
QY 4 DIVMTQSPSSLSVAGEKVTMSCKSSQSLNRSNKNYLAWYQOKPGQPPKLLIYGVFIR 63
Db 1 DIVMTQSPDSLAVSLGERATINCKASQSVND-----VAVYQKPGQSPKLLISYTSR 54
QY 64 DSGVPDRFTGSGSGTDTLTITSSVQAEADLAVYVCQNDHIYPYTFGGGTTKLEIK 116
Db 55 YAGVDPDRFSGSGSGTDTLTITSSVQAEADLAVYFCQDYNPSPTFGGTTKLEIK 107

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